

Epidemics on random intersection graphs

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Abstract

In this paper we consider a model for the spread of a stochastic SIR (Susceptible \rightarrow Infectious \rightarrow Recovered) epidemic on a network of individuals described by a random intersection graph. Individuals belong to a random number of cliques, each of random size, and infection can be transmitted between two individuals if and only if there is a clique they both belong to. Both the clique sizes and the number of cliques an individual belongs to follow mixed Poisson distributions. An infinite-type branching process approximation (with type being given by the length of an individual's infectious period) for the early stages of an epidemic is developed and made fully rigorous by proving an associated limit theorem as the population size tends to infinity. This leads to a threshold parameter R_* , so that in a large population an epidemic with few initial infectives can give rise to a large outbreak if and only if $R_* > 1$. A functional equation for the survival probability of the approximating infinite-type branching is determined; if $R_* \leq 1$, this equation has no non-zero solution, whilst, if $R_* > 1$, it is shown to have precisely one non-zero solution. A law of large numbers for the size of such a large outbreak is proved by exploiting a single-type branching process that approximates the susceptibility set of a typical individual.

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1 Introduction

Traditional models for the spread of SIR (Susceptible \rightarrow Infectious \rightarrow Recovered) epidemics [2, 15] are based on the homogeneous mixing assumption, that is, all pairs of individuals in the population contact each other at the same rate, independently of each other. Generalizations of this model have been proposed by introducing household structure into

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the population [4], where contacts between household members are more frequent than other contacts; by introducing a (social) network structure [1, 25], where contacts are only possible between pairs of individuals that share a connection in the network; or both [7, 8]. In most models for epidemics on networks, the network is modelled by a random graph constructed via the configuration model [23], [16, Chapter 3]. In this construction one can control the degree distribution of the vertices, but the resulting network is locally tree-like, in the sense that the network contains hardly any cliques (small completely connected groups) or short loops. In real social networks cliques are not sparse: ‘the friends of my friends are likely to be my friends as well’. This feature of networks has been captured (among other models, such as those in [30, 27, 17]) by random intersection graphs, introduced in [22] and further studied in e.g. [11, 14, 34] (see [10] for a related model). Random intersection graphs might be seen as models for overlapping groups/cliques, in which a contact between two individuals is possible only if there is a group to which they both belong. These graphs are also known as random key graphs in computer science [21] and are related to Rasch models [32] in the social sciences. In our paper, and in most random intersection graph models in the literature, the resulting graph still has a tree structure, though now at the level of cliques. This structure allows for analysis, but arguably only captures some features of real (social) networks. It is possible to make the graphs more realistic by incorporating spatial location [19], but this makes the model intractable for our purposes.

The aim of this paper is to study SIR epidemics on random intersection graphs. Specifically, we use branching process approximations to derive (i) a threshold parameter R_* , which determines whether an epidemic with few initial infectives can become established and infect a non-negligible proportion of the population, an event we call a large outbreak; (ii) the probability that a large outbreak occurs; and (iii) the fraction of the population that is infected by a large outbreak. These approximations are made fully rigorous as the population size tends to infinity by proving associated limit theorems.

The only previous rigorous study of epidemics on random intersection graphs is [11]. We extend the analysis of [11] in three directions. First, we allow more general distributions for both group size and the number of groups a typical individual belongs to. In [11], both of these quantities follow Poisson distributions; here we allow them to follow mixed-Poisson distributions. Moreover, as discussed in Section 6, we expect similar results to hold when they both follow quite general distributions, though our proofs are valid only for the mixed-Poisson case. Secondly, we allow for an arbitrary infectious period distribution, unlike in [11] where a Reed-Frost type model [2, Section 1.2] (which effectively has a constant infectious period) is used. Thirdly, we give a formal proof of a law of large numbers for the final outcome of a large outbreak, a result that was conjectured but not proved in [11]. Introducing variable infectious periods significantly complicates the analysis. We note that for random infectious periods, our model is not covered by [10, Section 5], since we need directed inhomogeneous random graphs and the proofs in [10] rely heavily on the structure of undirected graphs. Therefore, we need to develop alternative techniques to determine the fraction of the population that is infected by a large outbreak.

The remainder of the paper is organized as follows. Section 2 gives a brief introduction to random intersection graphs and SIR epidemics defined upon them. The main results of the paper, together with associated heuristic explanations, are given in Section 3. In

particular, in Section 3.2 we show how the early stages of an epidemic in our model can be approximated by a multitype (forward) branching process (whose type space is in general uncountable), yielding a threshold parameter R_* and the approximate probability of a large outbreak. In Section 3.3, a single-type (backward) branching process, which enables the proportion of the population that is infected by a large outbreak to be determined, is described. The key limit theorems of the paper are stated in Section 3.4. They show that, if there are few initial infectives, then in a large population: (i) a large outbreak can occur only if the forward branching process is supercritical; (ii) the probability that a large outbreak occurs is close to the probability that the forward branching process survives; and (iii) if there is a large outbreak, then the proportion of the population that is infected by the epidemic is close to the survival probability of the backward branching process. The forward multitype branching process is studied in Section 4, where it is shown that the process survives with non-zero probability if and only if $R_* > 1$ and that the survival probability may be obtained using a functional equation, which, as is proved in Appendix A, has at most one non-zero solution. The limit theorems corresponding to the forward and backward branching processes are proved in Sections 5.1 and 5.2, respectively. Extension to more general distributions of clique size and the number of groups a typical individual belongs to is discussed briefly in Section 6. Explicit expressions, in terms of Gontcharoff polynomials, for R_* and for the probability generating function(s) of the offspring distributions of the backward and forward branching processes (which enable the survival probabilities of these processes to be computed) are derived in Appendix B.

2 Epidemics and random intersection graphs

2.1 Notation

Throughout, \mathbb{N} denotes the set of natural numbers not including 0, while $\mathbb{Z}_+ = \mathbb{N} \cup \{0\}$. For $x \geq 0$, $\lfloor x \rfloor = \max(y \in \mathbb{Z}_+ : y \leq x)$ is the floor of x , and $\lceil x \rceil = \min(y \in \mathbb{Z}_+ : y \geq x)$ is the ceiling of x .

Furthermore, we write

$$\begin{aligned} f(x) = O(g(x)) & \quad \text{if} \quad \limsup_{x \rightarrow \infty} |f(x)/g(x)| < \infty, \\ f(x) = o(g(x)) & \quad \text{if} \quad \lim_{x \rightarrow \infty} f(x)/g(x) = 0 \quad \text{and} \\ f(x) = \Theta(g(x)) & \quad \text{if} \quad 0 < \liminf_{x \rightarrow \infty} |f(x)/g(x)| \leq \limsup_{x \rightarrow \infty} |f(x)/g(x)| < \infty. \end{aligned}$$

A (directed or undirected) graph is *simple* if it contains no parallel edges (edges that share both end-vertices) or self-loops (edges with only one end-vertex). In a directed graph, edges are parallel if they share both end-vertices and have the same direction. In a *multi-graph* self-loops and parallel edges are allowed. We may construct a directed graph from an undirected one by replacing every undirected edge by two directed edges with the same end-vertices but having opposite directions. If we construct a simple graph from a multi-graph, we do this by merging parallel edges and removing self-loops.

We use \mathbb{P} for general unspecified probability measures, for which the interpretation is clear from the context, and \mathbb{E} for the associated expectation. We use \mathbb{E}_X to denote

expectation with respect to the random variable X . However, if no confusion is possible we sometimes drop the subscript. For the non-negative random variable X , a mixed-Poisson(X) random variable, Y , is defined by $\mathbb{P}(Y = k) = \mathbb{E}_X[\frac{X^k}{k!}e^{-X}]$, for $k \in \mathbb{Z}_+$. We say that a random variable is $\mathcal{P}(x)$ if it is Poisson distributed with mean x and $\mathcal{MP}(X)$ if it has a mixed-Poisson(X) distribution. We use \tilde{X} to denote the size-biased variant of the non-negative random variable X , so, provided $\mathbb{E}[X] \in (0, \infty)$, for $x \geq 0$ we have

$$\mathbb{P}(\tilde{X} \leq x) = \frac{\int_{y \in [0, x]} y \mathbb{P}(X \in dy)}{\mathbb{E}[X]} = \frac{\mathbb{E}[X \mathbf{1}(X \leq x)]}{\mathbb{E}[X]}. \quad (2.1)$$

Here $\mathbf{1}(\mathcal{A})$, is the indicator function of \mathcal{A} , which is 1 if \mathcal{A} holds and 0 otherwise, and we assume that X is not almost surely 0. Note that if $Y \sim \mathcal{MP}(X)$, then $\tilde{Y} \sim \mathcal{MP}(\tilde{X}) + 1$; in this situation we use the notation \check{Y} to denote a random variable with the same distribution as $\tilde{Y} - 1$, so that if $Y \sim \mathcal{MP}(X)$, then $\check{Y} \sim \mathcal{MP}(\tilde{X})$. This implies that $\mathbb{E}[\check{Y}] = \mathbb{E}[\tilde{X}]$. Let $X_n \Rightarrow X$ denote convergence in distribution. By [18, Theorem 7.2.19] we know that if $X_n \Rightarrow X$, then $\mathbb{E}[X_n \mathbf{1}(X_n \leq x)] \rightarrow \mathbb{E}[X \mathbf{1}(X \leq x)]$ for all points of continuity of $\mathbb{P}(X \leq x)$. This implies that if $\mathbb{E}[X_n] \rightarrow \mathbb{E}[X]$ and $X_n \Rightarrow X$, then $\tilde{X}_n \Rightarrow \tilde{X}$.

We also use the notation $f_X(s) = \mathbb{E}[s^X]$ ($s \in [0, 1]$) for the probability generating function of a \mathbb{Z}_+ -valued random variable X and $\phi_X(\theta) = \mathbb{E}[e^{-\theta X}]$ ($\theta \geq 0$) for the moment generating function of a real-valued random variable X . Note that if $Y \sim \mathcal{MP}(X)$ then $\mathbb{E}[Y] = \mathbb{E}[X]$ and $f_Y(s) = \phi_X(1 - s)$. Lastly, for any set A we denote its cardinality by $|A|$.

2.2 Random intersection graphs

We consider a variant of random intersection graphs [11, 14, 22] constructed via a bipartite generalization of Norros and Reittu's Poissonian random graph model [28]. Random intersection graphs may be thought of as random graphs composed of overlapping groups/cliques of individuals/vertices. We note that the model introduced in [22] is more general than (the equal-weight variant of) the model presented in this paper.

We construct a sequence of random intersection graphs as follows. Consider two infinite sets of vertices $V = (v_i, i \in \mathbb{N})$ and $V' = (v'_j, j \in \mathbb{N})$. Fix a real number $\alpha > 0$. Assign independent and identically distributed (i.i.d.) weights $(A_i, i \in \mathbb{N})$ to the vertices in V , all distributed as the non-negative random variable A and, independently, i.i.d. weights $(B_j, j \in \mathbb{N})$ to the vertices in V' , all distributed as the non-negative random variable B . Assume that

$$\mu = \mathbb{E}[A] = \alpha \mathbb{E}[B] \in (0, \infty). \quad (2.2)$$

Define

$$L^{(n)} = \sum_{i=1}^n A_i, \quad (2.3)$$

$$L'^{(n)} = \sum_{j=1}^{\lfloor \alpha n \rfloor} B_j, \quad (2.4)$$

though see Remark 2.3 below. Let $(\Omega, \mathcal{F}, \nu)$ be the corresponding probability space, where $\Omega = (\mathbb{R}_+)^{\mathbb{N}} \times (\mathbb{R}_+)^{\mathbb{N}}$ is the product space of non-negative real-valued infinite sequences

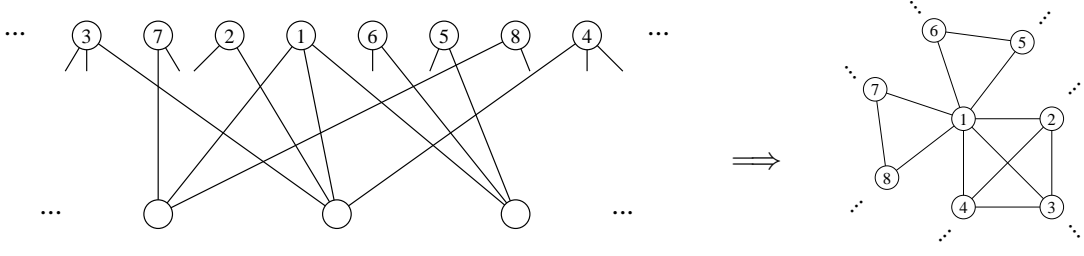


Figure 1: Construction of $G^{(n)}$ from $\mathbb{A}^{(n)}$.

$(A_i, i \in \mathbb{N})$ and $(B_j, j \in \mathbb{N})$. The σ -field \mathcal{F} is generated by the finite dimensional cylinders on Ω and ν is the appropriate (product) measure determined by the distributions of A and B . We note that, by the strong law of large numbers, both $L^{(n)}/(\mu n) \xrightarrow{a.s.} 1$ and $L'^{(n)}/(\mu n) \xrightarrow{a.s.} 1$ as $n \rightarrow \infty$. Here $\xrightarrow{a.s.}$ denotes almost sure convergence with respect to the measure ν .

For given $\omega \in \Omega$, an auxiliary sequence of random undirected multigraphs $(\mathbb{A}^{(n)}, n \in \mathbb{N}) = (\mathbb{A}^{(n)}(\omega), n \in \mathbb{N})$ is constructed as follows. For each n , the vertex set of $\mathbb{A}^{(n)}$ consists of $V^{(n)} = (v_i, 1 \leq i \leq n)$ and $V'^{(n)} = (v'_j, 1 \leq j \leq \lfloor \alpha n \rfloor)$. Vertices $v_i \in V^{(n)}$ and $v'_j \in V'^{(n)}$ share a $\mathcal{P}(A_i B_j / (\mu n))$ number of edges (see Remark 2.1). Conditioned on the weights of vertices, i.e. on ω , the numbers of edges between distinct pairs of vertices are independent and there is no edge in $\mathbb{A}^{(n)}$ connecting vertices either both in $V^{(n)}$ or both in $V'^{(n)}$. Note that in $\mathbb{A}^{(n)}$, the degree of vertex $v_i \in V^{(n)}$ is $\mathcal{P}(A_i^{(n)})$ with

$$A_i^{(n)} = A_i L'^{(n)} / (\mu n) \xrightarrow{a.s.} A_i \quad \text{as } n \rightarrow \infty, \quad (2.5)$$

while the degree of vertex $v'_j \in V'^{(n)}$ is $\mathcal{P}(B_j^{(n)})$ with

$$B_j^{(n)} = B_j L^{(n)} / (\mu n) \xrightarrow{a.s.} B_j \quad \text{as } n \rightarrow \infty. \quad (2.6)$$

The random variables $A^{(n)}$ and $B^{(n)}$ are defined by

$$\mathbb{P}(A^{(n)} \leq x) = n^{-1} |\{1 \leq i \leq n : A_i^{(n)} \leq x\}|, \quad (x \geq 0) \quad \text{and} \quad (2.7)$$

$$\mathbb{P}(B^{(n)} \leq x) = \lfloor \alpha n \rfloor^{-1} |\{1 \leq j \leq \lfloor \alpha n \rfloor : B_j^{(n)} \leq x\}|, \quad (x \geq 0). \quad (2.8)$$

Thus, $A^{(n)}(\omega)$ and $B^{(n)}(\omega)$ are random variables with the empirical distribution of the rescaled weights $\{A_i^{(n)}\}$ and $\{B_j^{(n)}\}$, respectively. By the strong law of large numbers, $A^{(n)} \Rightarrow A$ and $B^{(n)} \Rightarrow B$ as $n \rightarrow \infty$.

For the purpose of this paper it is not important how the graphs in the sequence depend on each other. For simplicity we assume that, conditioned on $\omega = (A_i, i \in \mathbb{N}) \times (B_j, j \in \mathbb{N})$, the graphs $(\mathbb{A}^{(n)}, n \in \mathbb{N})$ are independent.

The vertices of the random intersection graph $G^{(n)}$ are precisely those in $V^{(n)}$. Two (distinct) vertices share an edge in $G^{(n)}$ if and only if there is at least one path of length 2 between them in $\mathbb{A}^{(n)}$. Thus, $G^{(n)}$ is a simple graph. This construction is visualized in Figure 1. We note that $G^{(n)}$ is slightly different from an ordinary random intersection graph. In [11, 14] the conditional probability that vertices with weights A_i and B_j share an edge in $\mathbb{A}^{(n)}$ is given by $\min(1, A_i B_j / (\mu n))$, as opposed to $1 - \exp[-A_i B_j / (\mu n)]$ in this paper.

Remark 2.1. Of course it is possible to construct a simple version of the (multi) graph $\mathbb{A}^{(n)}$ directly, in which the vertices v_i and v'_j share an edge with probability $1 - \exp[-A_i B_j / (\mu n)]$. Indeed, this is sufficient to describe the population structure of our model. We use the present construction, where v_i and v_j share a Poisson distributed number of edges, in order to have the machinery ready for branching process approximations.

Remark 2.2. The graph $G^{(n)}$ is a graph of overlapping cliques, in which, asymptotically as $n \rightarrow \infty$, the number of cliques a vertex is part of has an $\mathcal{MP}(A)$ distribution and the clique sizes have an $\mathcal{MP}(B)$ distribution. Both of these distributions have finite mean by assumption.

Remark 2.3. Since the random intersection graph does not change if, for some $r \in (0, \infty)$, the random variables A and B are replaced by rA and B/r , condition (2.2) might be replaced by $\mathbb{E}[A] < \infty$ and $\mathbb{E}[B] < \infty$ but this does not gain any generality. The linear scaling $|V'^{(n)}| = \lfloor \alpha |V^{(n)}| \rfloor$ is assumed in order to guarantee that, as $n \rightarrow \infty$, (i) clique sizes do not grow to infinity, and (ii) two (or more) cliques contain at most one common vertex, with high probability.

Remark 2.4. In this paper we make use of the following equivalent way of constructing $\mathbb{A}^{(n)}$. Initially all vertices are unexplored. Pick a vertex from $V^{(n)}$ according to some law (e.g. uniformly at random), say vertex v_i , which has weight A_i ; this vertex becomes active. Assign a $\mathcal{P}(A_i^{(n)})$ number of edges to it (see (2.5)). The end-vertices in $V'^{(n)}$ of these edges are chosen independently with replacement and the probability that v'_j is chosen is $B_j / L'^{(n)}$. After this vertex v_i is made explored, while the chosen vertices become active.

Now, if there are any, explore the active vertices from $V'^{(n)}$ one by one. Suppose that we explore vertex v'_j , which has weight B_j ; then assign a $\mathcal{P}(B_j^{(n)})$ number of edges to it. These edges connect to vertices chosen independently, with replacement, from $V^{(n)}$; vertex v_l being chosen with probability $A_l / L^{(n)}$. If the end vertex has already been explored then the edge is ignored and not added to the graph, otherwise it is added and the end vertex in $V^{(n)}$ becomes active. If all the edges from v'_j are drawn, then v'_j is made explored.

The next step is to pick one of the active vertices from $V^{(n)}$, if there are any, according to some, for now unspecified, law and explore it. Say that we choose v_k , which has weight A_k . Then we proceed as in the first step. We assign a $\mathcal{P}(A_k^{(n)})$ number of edges to it, then the end-vertices in $V'^{(n)}$ of these edges are chosen independently with replacement and the probability that v'_j is chosen is $B_j / L'^{(n)}$. If the end vertex has been explored before, then the edge is ignored and deleted. After this, vertex v_k is made explored and the newly chosen vertices in $V'^{(n)}$ which are unexplored become active. We now explore all active vertices in $V'^{(n)}$ in turn, and so on until there is no active vertex left. After that an unexplored vertex from $V^{(n)}$ is chosen and the process goes on until all vertices in $V^{(n)}$ are explored. Note that if after this construction there are unexplored vertices left in $V'^{(n)}$, they will have degree 0, since there is no end-vertex left in $V^{(n)}$ to connect to.

2.3 SIR epidemics

We consider a stochastic SIR epidemic on the random intersection graph $G^{(n)}$. The vertices of the graph correspond to individuals and the edges to relationships/possible contacts. We assume that initially there is one infectious individual/vertex, chosen uniformly at random

from the population, while all other individuals are susceptible. Every individual, independently of other individuals, makes (directed) contact with each of its neighbours in $G^{(n)}$ at the points of independent Poisson processes of unit intensity. If an infectious individual contacts a susceptible one, the susceptible becomes infectious. Infectious individuals stay infectious for a random infectious period, distributed as \mathcal{I} , after which the infectious individual recovers and plays no further part in the epidemic. Infectious periods are i.i.d. and independent of the Poisson processes generating the contacts. An infectious contact is a contact by an infectious individual, irrespective of the state of the receiving individual. Note that there is no loss of generality in assuming that the intensity of the Poisson processes governing the contacts is 1, since this can always be achieved by rescaling time. We denote the above epidemic model by $\mathcal{E}^{(n)}(A, B, \mathcal{I})$.

For ease of exposition, primarily to avoid multitype branching processes that are reducible, we assume that $\mathbb{P}(\mathcal{I} = 0) = 0$. We omit the details but our results are readily extended to the case $\mathbb{P}(\mathcal{I} = 0) > 0$. Note, however, that we do allow for the possibility that $\mathbb{P}(\mathcal{I} = \infty) > 0$; if an infectious individual has infinite infectious period then, almost surely, that individual makes infectious contact with every member of each clique it belongs to.

In order to study properties of the epidemic on a graph, G say, we introduce the *Epidemic Generated Graph*, which is a directed graph constructed as follows. If G is undirected then make it directed by replacing every edge by two edges connecting the same vertices but in opposite directions. Assign every vertex i in G an independent realisation, x_i , of the random variable \mathcal{I} . Now thin G by deleting, independently, each edge emanating from vertex i with probability e^{-x_i} . Thus an edge starting at v_i is deleted if infection would not pass along it were v_i to become infected during the epidemic. The set of vertices that can be reached in the Epidemic Generated Graph from an initially infectious vertex v_0 (including v_0 itself) is distributed as the set of ultimately recovered individuals. The set of vertices from which there is a path in the Epidemic Generated Graph to vertex v_0 , including v_0 itself, is said to be the *susceptibility set* of v_0 [3, 5]. If one of the vertices in the susceptibility set of v_0 is the initially infectious individual, then v_0 will be ultimately recovered in the epidemic.

3 Main results and heuristics

3.1 Introduction

In this section we outline the main results of the paper, together with their heuristic explanations. In Section 3.2, we explain how the early stages of an SIR epidemic on a random intersection graph may be approximated by a (forward) branching process, yielding a threshold parameter R_* (see (3.1)) for the epidemic and the approximate probability that such an epidemic becomes established when the population size n is large. Unless the infectious period \mathcal{I} is constant, this branching process is multitype, its type space being the support of \mathcal{I} and hence in general uncountable. This infinite type branching process is studied separately in Section 4. In Section 3.3, we show how the susceptibility set of an individual may be approximated by a (backward) branching process, which is single-type even if \mathcal{I} is not constant. Furthermore, we explain why, if n is large, the proportion of the population that is ultimately infected by an epidemic that becomes established is

approximately the probability that the backward branching process avoids extinction. The above approximations are made fully rigorous by considering SIR epidemics on a sequence of random intersection graphs, indexed by the population size n , and proving associated limit theorems. These theorems are stated in Section 3.4 and proved in Section 5. Calculation of extinction probabilities for the forward and backward branching processes requires exact results concerning the final outcome and susceptibility sets for standard SIR epidemics in closed homogeneously mixing populations, which are given in Appendix B.

3.2 Early stages of an epidemic

3.2.1 Fixed infectious period

Consider the epidemic model $\mathcal{E}^{(n)}(A, B, \mathcal{I})$ defined in Section 2.3 and, for simplicity, suppose first that the infectious period is constant, i.e. there exists $\iota > 0$ such that $\mathbb{P}(\mathcal{I} = \iota) = 1$. In the limit as the population size $n \rightarrow \infty$, the initial infective, i^* say, belongs to $X \sim \mathcal{MP}(A)$ cliques, having sizes $\check{Y}_1 + 1, \check{Y}_2 + 1, \dots, \check{Y}_X + 1$, where, given X , the random variables $\check{Y}_1, \check{Y}_2, \dots, \check{Y}_X$ are mutually independent and $(\check{Y}_i | X) \sim \mathcal{MP}(\tilde{B})$ ($i = 1, 2, \dots, X$). The size biasing comes in because the probability of being part of a clique is proportional to its weight. Moreover, apart from i^* , these cliques are almost surely disjoint as $n \rightarrow \infty$. The initial infective will trigger a local (within-clique) epidemic in each of the X cliques it belongs to. The group of initial susceptibles in a single clique that are infected through a local epidemic started by i^* is called a *litter* of i^* . (Note that a litter may be empty, i.e. if no susceptible in the corresponding clique is infected.) Let $T(m)$ denote the size of a litter, not counting the initial infective i^* , given that the clique has size $m + 1$. (We call $T(m)$ the size of a local epidemic or the size of a litter.) Then the total number of individuals infected (excluding i^*) by the local epidemics in the cliques that i^* belongs to is distributed as

$$C^f = \sum_{i=1}^X T(\check{Y}_i),$$

where $T(\check{Y}_1), T(\check{Y}_2), \dots, T(\check{Y}_X)$ are independent, since the infectious period is constant.

Now consider a typical individual, j^* say, that is part of one of the litters of i^* . In the limit as $n \rightarrow \infty$, (i) individual j^* belongs to $\check{X} \sim \mathcal{MP}(\tilde{A})$ cliques, in addition to the clique j^* was infected through (i.e. the one also containing i^*), having sizes distributed independently as $\mathcal{MP}(\tilde{B}) + 1$ and (ii) apart from j^* , the $\check{X} + 1$ cliques containing j^* are disjoint. (The size biasing here arises because, in the construction of $G^{(n)}$, the probability that a vertex joins a given clique is proportional to the weight of that vertex; see Remark 2.4.) Individual j^* will trigger a local epidemic in each of the \check{X} ‘new’ cliques it belongs to. The total number of individuals infected (excluding j^*) in these \check{X} local epidemics (the sum of the sizes of the litters of j^*) is distributed as

$$\tilde{C}^f = \sum_{i=1}^{\check{X}} T(\check{Y}_i),$$

where, given \check{X} , the random variables $T(\check{Y}_1), T(\check{Y}_2), \dots, T(\check{Y}_{\check{X}})$ are independent.

The construction of the epidemic process may be continued in the obvious fashion. It follows that, if the population size n is large, the number of infected individuals in the early

stages of the epidemic process may be approximated by a (Galton-Watson) branching process, with one initial ancestor, and offspring distribution that of C^f in the initial generation and of \tilde{C}^f in all subsequent generations. This approximation is made precise by using a coupling argument in Section 5.1. The coupling between the epidemic and branching processes breaks down when a clique used to spread a local epidemic intersects a previously used clique, which, with probability tending to one as $n \rightarrow \infty$, happens if and only if the branching process does not go extinct.

Let

$$R_* = \mathbb{E}[\tilde{C}^f] = \mathbb{E}_{\tilde{Y}}[\mathbb{E}[T(\tilde{Y})|\tilde{Y}]]\mathbb{E}[\tilde{X}] = \mathbb{E}_{\tilde{Y}}[\mathbb{E}[T(\tilde{Y})|\tilde{Y}]]\mathbb{E}[\tilde{A}] \quad (3.1)$$

and, for $s \in [0, 1]$, let

$$f_{C^f}(s) = \mathbb{E}[s^{C^f}] = f_X(\mathbb{E}_{\tilde{Y}}[f_{T(\tilde{Y})|\tilde{Y}}(s)])$$

and

$$f_{\tilde{C}^f}(s) = \mathbb{E}[s^{\tilde{C}^f}] = f_{\tilde{X}}(\mathbb{E}_{\tilde{Y}}[f_{T(\tilde{Y})|\tilde{Y}}(s)]).$$

Let ρ be the survival probability of the above branching process (i.e. the probability that it does not go extinct). Then, by standard branching process theory [20], if $R_* \leq 1$ then $\rho = 0$ and if $R_* > 1$ then

$$\rho = 1 - f_{C^f}(\sigma), \quad (3.2)$$

where σ is the unique solution in $[0, 1)$ of the equation

$$f_{\tilde{C}^f}(s) = s. \quad (3.3)$$

The coupling of the epidemic and branching processes mentioned above implies that, if the population size n is suitably large, R_* is a threshold parameter for the epidemic process and the probability that an epidemic initiated by a single infective becomes established and leads to a major outbreak is given approximately by ρ . Note that in [11], the notation R_0 is used instead of R_* . We use the notation of [7, 8], because R_0 is usually defined as the expected number of new *direct* infections caused by an infectious individual in the first stages of an epidemic [2, 15, 29], while in (3.1) *all* individuals infected by a local epidemic are ‘assigned to’ the initial infectious individual in the clique.

3.2.2 General infectious period distribution

When the infectious period is not constant we can still approximate the epidemic $\mathcal{E}^{(n)}(A, B, \mathcal{I})$ by considering successive local epidemics as above, but the approximating process is no longer a simple single-type branching process. There are two reasons for this. First, the sizes of the litters of an individual, i^* say, are not independent since the infectious period of the initial infective in the corresponding cliques is the same (i.e. the infectious period of i^*). Secondly, the infectious periods of infectives in a litter are not independent of the size of that litter. These difficulties may be overcome by considering a multitype branching process, in which individuals are typed by the length of their infectious period. If the infectious period \mathcal{I} has finite support then standard finite-type branching process theory (see e.g. [20, Chapter 4]) may be used, so we now assume that \mathcal{I} has infinite (possibly uncountable) support.

In view of these observations, we approximate the early stages of the epidemic $\mathcal{E}^{(n)}(A, B, \mathcal{I})$ by a multitype branching process

$$\mathcal{Z}^f = \mathcal{Z}^f(A, B, \mathcal{I}) = (\mathcal{Z}_i^f, i \in \mathbb{Z}_+),$$

defined as follows. The type space is $(0, \infty]$, with the type of an individual being given by the infectious period of the corresponding individual in the epidemic process. For $i \in \mathbb{Z}_+$, \mathcal{Z}_i^f is a multiset of points in $(0, \infty]$ giving the types of individuals present in generation i of the branching process. (Note that if the distribution of \mathcal{I} has atoms, at infinity or otherwise, then \mathcal{Z}_i^f may contain repeated elements; on the other hand if the distribution of \mathcal{I} is continuous then, almost surely, all elements of \mathcal{Z}_i^f are distinct and hence \mathcal{Z}_i^f is a set.) There is one initial ancestor, corresponding to the initial infective, i^* say, in the epidemic $\mathcal{E}^{(n)}(A, B, \mathcal{I})$ and its type is distributed as \mathcal{I} . As in the constant infectious period case, i^* belongs to $X \sim \mathcal{MP}(A)$ cliques, having sizes distributed independently as $\check{Y} + 1$, where $\check{Y} \sim \mathcal{MP}(\tilde{B})$, and in \mathcal{Z}^f , the offspring of the initial ancestor corresponds to all the individuals infected in the local epidemics triggered by i^* in these X cliques, though now of course we also keep track of their types (infectious periods). In the branching process, a group of children corresponding to a litter in the epidemic process is also referred to as a litter. The offspring of any individuals in a non-initial generation of \mathcal{Z}^f are defined in a similar fashion, except X is replaced by $\check{X} \sim \mathcal{MP}(\tilde{A})$. Of course, the offspring of distinct individuals in \mathcal{Z}^f are mutually independent.

The branching process \mathcal{Z}^f , which we call a forward branching process because it approximates the forward spread of the epidemic $\mathcal{E}^{(n)}(A, B, \mathcal{I})$, is analysed in Section 4. Let $\tilde{\mathcal{Z}}^f$ be the multitype branching process defined analogously to \mathcal{Z}^f , except the offspring distribution in all generations of $\tilde{\mathcal{Z}}^f$ is that of the non-initial generations in \mathcal{Z}^f . Let ρ be the probability that \mathcal{Z}^f survives and, for $x \in (0, \infty]$, let $\tilde{\rho}(x)$ be the probability that $\tilde{\mathcal{Z}}^f$ survives given that the ancestor has type x . Let R_* be defined as in (3.1), where $T(m)$ is distributed as the size of a local epidemic, initiated by a single infective in a clique of size $m + 1$, in which the infectious periods of infectives (including the initial one) are i.i.d. copies of \mathcal{I} . (An expression for $\mathbb{E}_{\check{Y}}[\mathbb{E}[T(\check{Y})|\check{Y}]]$ is given by equation (B.7) in Appendix B.2, thus enabling R_* to be computed.) Then $\rho > 0$ if and only if $R_* > 1$ (see Theorem 4.2), so R_* is still a threshold parameter for the epidemic. Also, when $R_* > 1$, ρ is given by an infinite-type analogue of (3.2); see (4.4), which expresses ρ as the expectation of a functional of $\tilde{\rho}$ with respect to the distribution \mathcal{I} of x . Furthermore, $\tilde{\rho}$ satisfies a functional equation (see (4.3)), which is essentially an infinite-type analogue of (3.3) and has at most one non-zero solution (see Lemma 4.1).

3.3 Final outcome of an epidemic

Recall the definition of the susceptibility set of an individual given in Section 2.3. We require also the concept of a *local susceptibility set*, which is defined in exactly the same way as a susceptibility set but for an epidemic on a single clique. For $m = 0, 1, \dots$, let $S(m)$ denote the size of a typical local susceptibility set of an individual in a clique of size $m + 1$, where $S(m)$ does not include the individual itself.

We may approximate the early growth of a susceptibility set of an individual, i^* say, by a branching process in much the same way as we did for the early stages of an epidemic. We

consider first those individuals, not including i^* itself, who belong to a local susceptibility set of i^* . These are the offspring of i^* in the branching process. We next repeat this process for each individual, j^* say, in the first generation of the branching process to obtain the second generation, and so on. This leads to a (backward) branching process

$$\mathcal{Z}^b = \mathcal{Z}^b(A, B, \mathcal{I}) = (\mathcal{Z}_i^b, i \in \mathbb{Z}_+)$$

having one initial ancestor, in which the number of offspring of the ancestor is distributed as

$$C^b = \sum_{i=1}^X S(\check{Y}_i),$$

and the number of offspring of any subsequent individual is distributed as

$$\tilde{C}^b = \sum_{i=1}^{\tilde{X}} S(\check{Y}_i),$$

where $X, \tilde{X}, \check{Y}_1, \check{Y}_2, \dots$ are independent, $X \sim \mathcal{MP}(A)$, $\tilde{X} \sim \mathcal{MP}(\tilde{A})$ and $\check{Y}_i \sim \mathcal{MP}(\tilde{B})$ ($i = 1, 2, \dots$).

Note that the local susceptibility set of an individual is independent of its infectious period, so \mathcal{Z}^b is a single-type branching process; thus \mathcal{Z}_i^b is determined by its cardinality $|\mathcal{Z}_i^b|$, in contrast to \mathcal{Z}_i^f (which is single-type only if \mathcal{I} is almost surely equal to a fixed constant).

Let

$$R_*^b = \mathbb{E}[\tilde{C}^b] = \mathbb{E}_{\check{Y}}[\mathbb{E}[S(\check{Y})|\check{Y}]]\mathbb{E}[\tilde{A}] \quad (3.4)$$

be the mean number of children of an individual in \mathcal{Z}^b who is not the ancestor and, for $s \in [0, 1]$, define the probability generating functions

$$f_{C^b}(s) = \mathbb{E}[s^{C^b}] = f_X(\mathbb{E}_{\check{Y}}[f_{S(\check{Y})|\check{Y}}(s)])$$

and

$$f_{\tilde{C}^b}(s) = \mathbb{E}[s^{\tilde{C}^b}] = f_{\tilde{X}}(\mathbb{E}_{\check{Y}}[f_{S(\check{Y})|\check{Y}}(s)]).$$

Denote by $\rho^b = \rho^b(A, B, \mathcal{I})$ the survival probability of \mathcal{Z}^b . Then, by standard branching process theory, if $R_*^b \leq 1$ then $\rho^b = 0$ and if $R_*^b > 1$ then

$$\rho^b = 1 - f_{C^b}(\xi), \quad (3.5)$$

where ξ is the unique solution in $[0, 1)$ of the equation

$$f_{\tilde{C}^b}(s) = s. \quad (3.6)$$

Note that an expression for $\mathbb{E}_{\check{Y}}[f_{S(\check{Y})|\check{Y}}(s)]$ is given by equation (B.8) in Appendix B.2, which enables ρ^b to be computed. In connection with this computation, also recall that $f_X(s) = \phi_A(1 - s)$ and observe that $f_{\tilde{X}}(s) = \phi_{\tilde{A}}(1 - s) = -\phi'_A(1 - s)/\mathbb{E}[A]$, where ϕ'_A is the derivative of ϕ_A .

Before describing how the backward branching process \mathcal{Z}^b is used to study the final outcome of an epidemic in a large population; we briefly discuss the relationship between the forward and backward branching processes. In particular we note two important consequences of this relationship.

Remark 3.1. Let G' be the Epidemic Generated Graph (see Section 2.3) for an epidemic on a single clique (G say) of $m + 1$ individuals, labelled $0, 1, \dots, m$. For distinct $i, j \in \{0, 1, \dots, m\}$, let $\chi_{i,j} = 1$ if there is a chain of directed edges from i to j in G' and let $\chi_{i,j} = 0$ otherwise. Then $T(m)$ and $S(m)$ are distributed as $\sum_{i=1}^m \chi_{0,i}$ and $\sum_{i=1}^m \chi_{i,0}$, respectively, so by symmetry, $\mathbb{E}[T(m)] = m\mathbb{P}(\chi_{0,1} = 1)$ and $\mathbb{E}[S(m)] = m\mathbb{P}(\chi_{1,0} = 1)$. Further, by symmetry, $\mathbb{P}(\chi_{0,1} = 1) = \mathbb{P}(\chi_{1,0} = 1)$, and it follows from (3.1) and (3.4) that $R_*^b = R_*$. Thus we use only the notation R_* .

Remark 3.2. Consider the graphs G and G' of the previous remark, and suppose that the infectious period \mathcal{I} is constant, say $\mathbb{P}(\mathcal{I} = \iota) = 1$. Then G' is obtained from the directed version of G by deleting directed edges independently, each with probability $e^{-\iota}$. Thus, if G'' is obtained from G' by reversing the direction of all arrows, then G'' and G' are identically distributed, whence so are $T(m)$ and $S(m)$. It follows that in this case $\rho^b = \rho$. This argument breaks down when \mathcal{I} is not constant. In that case, apart from the branching process \mathcal{Z}^f being multitype, the directed edges from a given vertex in G' are not independent, whence $T(m)$ and $S(m)$ have different distributions. Thus generally $\rho^b \neq \rho$.

Now we describe the relationship between the backward branching process and the final outcome of an epidemic. Consider the epidemic model $\mathcal{E}^{(n)}(A, B, \mathcal{I})$ and suppose that the population size n is large. Choose an initially susceptible individual uniformly at random from all initial susceptibles, j say, and construct its susceptibility set on a generation basis as described above for \mathcal{Z}^b . Stop this construction when the total size of the susceptibility set becomes greater than $\log n$ or when the susceptibility set process goes extinct, whichever occurs first. The susceptibility set process can be coupled to the backward branching process \mathcal{Z}^b so that, with probability tending to 1 as $n \rightarrow \infty$, the two coincide whilst their sizes are not greater than $\log n$. Also, the probability that the total progeny of \mathcal{Z}^b is greater than $\log n$ tends to ρ^b as $n \rightarrow \infty$.

By symmetry, the initial infective in $\mathcal{E}^{(n)}(A, B, \mathcal{I})$, i say, may be chosen by picking an individual uniformly at random from the population excluding j . Thus, if j 's susceptibility set process goes extinct before reaching size $\log n$ then the probability that j 's susceptibility set contains the initial infective (and hence that j is ultimately infected by the epidemic) tends to zero as $n \rightarrow \infty$. Suppose instead that j 's susceptibility set process does reach size $\log n$. Then we choose the initial infective i as above, construct the forward epidemic process from i and determine whether or not the latter intersects the $\log n$ individuals in j 's partially constructed susceptibility set. If it does then j is ultimately infected by the epidemic, otherwise j remains uninfected.

Recall that the forward epidemic process originating from i is approximated by the branching process \mathcal{Z}^f . If \mathcal{Z}^f goes extinct then, in the limit as $n \rightarrow \infty$, there are only finitely many individuals infected in the epidemic and hence the probability that the epidemic intersects j 's partially constructed susceptibility set tends to zero. If \mathcal{Z}^f does not go extinct then, by exploiting a lower bounding branching process for the epidemic process, we show in Section 5.2 that, as $n \rightarrow \infty$, the epidemic process almost surely infects $\Theta(n)$ individuals and hence the probability that it intersects j 's partially constructed susceptibility set tends to one.

The above implies that the asymptotic probability that an initial susceptible, chosen uniformly at random, is ultimately infected by a major outbreak is ρ^b . Hence the asymptotic expected proportion of the population ultimately infected by a major outbreak is also ρ^b .

Now consider two distinct initial susceptibles chosen uniformly at random, j_1 and j_2 say, and construct their susceptibility sets on a generation basis as above, stopping each process if its size reaches $\log n$ or if the process goes extinct. The two partially constructed susceptibility set processes are asymptotically independent as $n \rightarrow \infty$, which enables a weak law of large numbers to be proved for the proportion of the population that is ultimately infected by a major outbreak.

3.4 Limit theorems for SIR epidemics on random intersection graphs

Let $\mathcal{R}^{(n)} = \mathcal{R}^{(n)}(A, B, \mathcal{I})$ be the set of ultimately recovered vertices, including the single initial infective, in the SIR epidemic $\mathcal{E}^{(n)}(A, B, \mathcal{I})$ on the random intersection graph $G^{(n)}$, constructed using the infectious period distribution \mathcal{I} and the sequences $(A_i, i \in \mathbb{N})$, $(B_j, j \in \mathbb{N})$ (as described in Section 2.2). Our focus is on the properties of $|\mathcal{R}^{(n)}|$, the number of ultimately recovered individuals in the epidemic. For a branching process, \mathcal{Z}^f say, let $|\mathcal{Z}^f| = \sum_{i=0}^{\infty} |\mathcal{Z}_i^f|$ denote its total size (total progeny), including the ancestor. Recall that $\mathcal{Z}^f = \mathcal{Z}^f(A, B, \mathcal{I})$ and $\mathcal{Z}^b = \mathcal{Z}^b(A, B, \mathcal{I})$ are the (forward and backward) branching processes, which approximate the epidemic process and the process exploring a susceptibility set, respectively. Recall also that ρ and ρ^b are their respective survival probabilities.

Our first theorem establishes the precise sense in which the forward process approximates the early stages of an epidemic.

Theorem 3.3. *For all $k \in \mathbb{N}$,*

$$\lim_{n \rightarrow \infty} \mathbb{P}(|\mathcal{R}^{(n)}| = k) = \mathbb{P}(|\mathcal{Z}^f| = k).$$

The next result establishes the connection between the backward process and the proportion of individuals ultimately infected.

Theorem 3.4. *For every $0 < \epsilon < \rho^b$,*

$$\lim_{n \rightarrow \infty} \mathbb{P}\left(\left|\frac{|\mathcal{R}^{(n)}|}{n} - \rho^b\right| < \epsilon\right) = \rho.$$

Theorems 3.3 and 3.4 are proved in Sections 5.1 and 5.2, respectively. Finally, we use these two results to establish the following convergence in distribution of the proportion of individuals ultimately infected in the epidemic process.

Theorem 3.5. *Let T_F be a random variable with $\mathbb{P}(T_F = \rho^b) = \rho = 1 - \mathbb{P}(T_F = 0)$. Then, as $n \rightarrow \infty$,*

$$n^{-1}|\mathcal{R}^{(n)}| \Rightarrow T_F.$$

Proof. First note that Theorem 3.3 implies that, for any $\epsilon > 0$ and any $k \in \mathbb{N}$,

$$\liminf_{n \rightarrow \infty} \mathbb{P}(n^{-1}|\mathcal{R}^{(n)}| \leq \epsilon) \geq \mathbb{P}(|\mathcal{Z}^f| \leq k),$$

whence, letting $k \rightarrow \infty$,

$$\liminf_{n \rightarrow \infty} \mathbb{P}(n^{-1}|\mathcal{R}^{(n)}| \leq \epsilon) \geq 1 - \rho. \quad (3.7)$$

Suppose that $R_* \leq 1$. Then $\rho = 0$ and (3.7) implies that

$$n^{-1}|\mathcal{R}^{(n)}| \Rightarrow 0 \quad \text{as } n \rightarrow \infty. \quad (3.8)$$

On the other hand, suppose that $R_* > 1$, so $\rho > 0$. Then Theorem 3.4 implies that, for $0 < \epsilon < \rho^b$, $\limsup_{n \rightarrow \infty} \mathbb{P}(n^{-1}|\mathcal{R}^{(n)}| \leq \epsilon) \leq 1 - \rho$, which, together with (3.7), yields that, for such ϵ ,

$$\lim_{n \rightarrow \infty} \mathbb{P}(n^{-1}|\mathcal{R}^{(n)}| \leq \epsilon) = 1 - \rho.$$

The theorem then follows upon combining this observation with (3.8) and Theorem 3.4. \square

4 Properties of the forward branching process

In this section we study the survival probability of the branching process \mathcal{Z}^f introduced in Section 3.2. Recall that individuals in \mathcal{Z}^f are typed by the length of the infectious period of the corresponding individual in the epidemic process. There is one ancestor, i^* say, whose type is distributed as \mathcal{I} and who belongs to $X \sim \mathcal{MP}(A)$ cliques. (That is, the corresponding individual in the epidemic process $\mathcal{E}^{(n)}(A, B, \mathcal{I})$ belongs to $X \sim \mathcal{MP}(A)$ cliques.) Those cliques have sizes that are independent and identically distributed as $1 + \tilde{Y}$, where $\tilde{Y} \sim \mathcal{MP}(\tilde{B})$. The offspring of the ancestor correspond to the individuals who are infected, in the corresponding epidemic process, by the local epidemics triggered by i^* in the X cliques it belongs to. The offspring of i^* are grouped into litters with each litter corresponding to a clique of i^* . Note that some litters might be empty (if the epidemic fails to spread further into some cliques to which i^* belongs). The offspring of any subsequent individual is defined similarly, except that such an individual belongs to $\tilde{X} \sim \mathcal{MP}(\tilde{A})$ cliques in addition to the clique it was infected through. The type space for \mathcal{Z}^f is given by the support of \mathcal{I} , which is a subset of $(0, \infty]$. For ease of exposition, we assume that \mathcal{I} has support $(0, \infty]$; extension to other cases is straightforward.

We investigate the survival probability of \mathcal{Z}^f using functionals defined on measurable test functions $h : (0, \infty] \rightarrow [0, 1]$ as follows (cf. [9, 10]). Let $h(x)$ be a given test function. Suppose that individuals in \mathcal{Z}^f are marked independently, with an individual of type x being marked with probability $h(x)$. Let $F(h)(x)$ be the probability that an ancestor of type x has at least one marked child in a given litter and let $\Phi(h)(x)$ be the probability that an ancestor of type x has at least one marked child. Recall that the probability generating function of X is given by $f_X(s) = \phi_A(1 - s)$ ($s \in [0, 1]$), where $\phi_A(\theta) = \mathbb{E}[e^{-\theta A}]$ is the moment generating function of A . It follows that

$$\Phi(h)(x) = 1 - \phi_A(F(h)(x)). \quad (4.1)$$

Define the functional $\tilde{\Phi}(h)(x)$ similarly for the branching process $\tilde{\mathcal{Z}}^f$, defined in the final paragraph of Section 3.2.2; thus

$$\tilde{\Phi}(h)(x) = 1 - \phi_{\tilde{A}}(F(h)(x)). \quad (4.2)$$

Let ρ_i be the probability that generation i of the branching process \mathcal{Z}^f is non-empty, that is $\rho_i = \mathbb{P}(|\mathcal{Z}_i^f| > 0)$. By definition ρ_i is non-increasing, so $\rho = \lim_{i \rightarrow \infty} \rho_i$ exists and is the probability of survival of the branching process. Let $\tilde{\rho}_i(x)$ be the probability

that the lineage of an individual (i.e. the sub-process consisting of that individual and all its descendants), which is not the ancestor and has type x , survives for at least i further generations and let $\tilde{\rho}(x) = \lim_{i \rightarrow \infty} \tilde{\rho}_i(x)$ be the probability that this lineage survives forever. Note that $\tilde{\rho}_1(x) = \tilde{\Phi}(\mathbf{1})(x)$, where $\mathbf{1}$ is the function which is equal to 1 on its entire domain. It is clear that $\tilde{\rho}(x)$ satisfies

$$\tilde{\rho}(x) = \tilde{\Phi}(\tilde{\rho})(x), \quad (4.3)$$

since in order for the lineage of an individual to survive, at least one of the children of that individual must have a surviving lineage. Furthermore,

$$\rho = \int_{(0, \infty]} \Phi(\tilde{\rho})(x) \mathbb{P}(\mathcal{I} \in dx) = \mathbb{E}[\Phi(\tilde{\rho})(\mathcal{I})]. \quad (4.4)$$

Let $\tilde{\Phi}_i$ be the i -th iterate of $\tilde{\Phi}$ and note that $\tilde{\rho}_i(x) = \tilde{\Phi}_i(\mathbf{1})(x)$. The functionals $\Phi(h)(x)$ and $\tilde{\Phi}(h)(x)$ are monotonic increasing in $h(x)$. Therefore, $\tilde{\rho}(x) = \lim_{i \rightarrow \infty} \tilde{\Phi}_i(\mathbf{1})(x)$ is the pointwise maximal solution of (4.3). Note that, since \mathcal{Z}^f is irreducible, either $\tilde{\rho}(x) = 0$ for all $x \in (0, \infty]$ or $\tilde{\rho}(x) > 0$ for all $x \in (0, \infty]$. The following lemma is proved and discussed in Appendix A.

Lemma 4.1. *There is at most one non-zero solution $\tilde{\rho}(x)$ of (4.3).*

Now recall the definition of R_* from (3.1), where $\check{Y} \sim \mathcal{MP}(\tilde{B})$ and as before let $T(m)$ denote the size of a litter, in a clique of m initial susceptibles, in which the infectious periods of infectives are i.i.d. copies of \mathcal{I} . It is convenient here to show explicitly the dependence on \mathcal{I} and write $T(m) = T(m, \mathcal{I})$, so

$$R_* = \mathbb{E}_{\check{Y}}[\mathbb{E}[T(\check{Y}, \mathcal{I}) | \check{Y}]] \mathbb{E}[\tilde{A}].$$

Theorem 4.2. *The survival probability satisfies $\rho > 0$ if and only if $R_* > 1$.*

Proof. Suppose first that $R_* > 1$. For $k \in \mathbb{Z}_+$, let $L(k, \mathcal{I}) = \mathbb{E}[T(\check{Y}, \mathcal{I}) | \check{Y} = k]$. Then there exists $K \in \mathbb{N}$ such that

$$\mathbb{E}[\tilde{A}] \sum_{k=0}^K L(k, \mathcal{I}) \mathbb{P}(\check{Y} = k) > 1. \quad (4.5)$$

For $\epsilon > 0$, let \mathcal{I}_ϵ be the discrete random variable obtained from \mathcal{I} by $\mathcal{I}_\epsilon = \epsilon \lfloor \mathcal{I}/\epsilon \rfloor$ (with the convention that $\lfloor \infty \rfloor = \infty$) and note that \mathcal{I}_ϵ is stochastically smaller than \mathcal{I} . Since $L(k, \mathcal{I})$ depends on the realisation of an Epidemic Generated Graph defined on a finite clique, there exists $\epsilon > 0$ such that

$$\mathbb{E}[\tilde{A}] \sum_{k=0}^K L(k, \mathcal{I}_\epsilon) \mathbb{P}(\check{Y} = k) > 1.$$

Analagously to the derivation of (4.5), there exists $K'_\epsilon \in \mathbb{N}$ such that for $\mathcal{I}'_\epsilon = \mathcal{I}_\epsilon \mathbf{1}(\mathcal{I}_\epsilon \notin (K'_\epsilon, \infty))$, we have

$$\mathbb{E}[\tilde{A}] \sum_{k=0}^{K'_\epsilon} L(k, \mathcal{I}'_\epsilon) \mathbb{P}(\check{Y} = k) > 1. \quad (4.6)$$

Consider the branching process $\tilde{\mathcal{Z}}^f(A, B, \mathcal{I}'_\epsilon)$, which has finitely many types and is irreducible. Let \tilde{M} be the mean offspring matrix of $\tilde{\mathcal{Z}}^f(A, B, \mathcal{I}'_\epsilon)$. Note that whether or not an individual in a clique becomes infected is independent of that individual's own infectious period. It follows that the rows of \tilde{M} are each proportional to the probability mass function of \mathcal{I}'_ϵ , so \tilde{M} has rank one and the maximal eigenvalue of \tilde{M} is given by its trace, which is easily seen to be equal to the left hand side of (4.6). Therefore, if $R_* > 1$, the branching process $\tilde{\mathcal{Z}}^f(A, B, \mathcal{I})$ dominates the irreducible finite-type supercritical branching process $\tilde{\mathcal{Z}}^f(A, B, \mathcal{I}'_\epsilon)$, which we know from standard theory [20, Theorem 4.2.2] has a strictly positive probability of survival. Thus $\tilde{\rho}(x) > 0$ for all $x \in (0, \infty]$; equation (4.4) then implies that $\rho > 0$.

For $R_* \leq 1$ we use a similar argument to [10]. Suppose that $R_* \leq 1$ and that $\tilde{\rho}(x) > 0$ for some (and thus all) $x \in (0, \infty]$. Recall that $\tilde{\Phi}(\tilde{\rho})(x)$ is the probability that, in $\tilde{\mathcal{Z}}^f(A, B, \mathcal{I})$ and with individuals of type x being marked with probability $\tilde{\rho}(x)$, an individual of type x has at least one marked child. Note that this probability is strictly smaller than the expectation of the number, $T_M(x, \tilde{\rho})$ say, of marked children of such an individual. Let $T(x, m, \mathcal{I})$ denote the size of a single-clique epidemic with m initial susceptibles and a single initial infective which has infectious period x . Then, again exploiting the fact that whether or not an individual is infected is independent of its infectious period, we find that

$$\mathbb{E}[T_M(x, \tilde{\rho})] = \mathbb{E}[\tilde{A}] \mathbb{E}_{\tilde{Y}}[\mathbb{E}[T(x, \tilde{Y}, \mathcal{I}) | \tilde{Y}]] \mathbb{E}[\tilde{\rho}(\mathcal{I})],$$

whence, recalling (4.3),

$$\tilde{\rho}(x) = \tilde{\Phi}(\tilde{\rho})(x) < \mathbb{E}[\tilde{A}] \mathbb{E}_{\tilde{Y}}[\mathbb{E}[T(x, \tilde{Y}, \mathcal{I}) | \tilde{Y}]] \mathbb{E}[\tilde{\rho}(\mathcal{I})]. \quad (4.7)$$

Note that if x is a realisation of a random variable \mathcal{I}_0 that is distributed as \mathcal{I} , then $\mathbb{E}[T(m, \mathcal{I})] = \mathbb{E}_{\mathcal{I}_0}[\mathbb{E}[T(\mathcal{I}_0, m, \mathcal{I}) | \mathcal{I}_0]]$ and (4.7) implies that $\mathbb{E}[\tilde{\rho}(\mathcal{I})] < R_* \mathbb{E}[\tilde{\rho}(\mathcal{I})]$. It then follows that $R_* > 1$, which is a contradiction. Thus, if $R_* \leq 1$ then $\tilde{\rho}(x)$ is identically zero on the support of \mathcal{I} and it then follows from (4.4) that $\rho = 0$. \square

5 Proofs

In this section we give formal proofs of Theorems 3.3 and 3.4. Recall the probability space $(\Omega, \mathcal{F}, \nu)$ defined in Section 2.2, where Ω is the product space of non-negative real-valued infinite sequences $(A_i, i \in \mathbb{N})$ and $(B_j, j \in \mathbb{N})$ and ν is the appropriate (product) measure determined by the distributions of A and B . In the proofs we consider processes which depend on $\omega \in \Omega$, that is on the sequences $(A_i, i \in \mathbb{N})$ and $(B_i, i \in \mathbb{N})$. The measure governing a process conditioned on ω is denoted by \mathbb{P}_ω and the corresponding expectation by \mathbb{E}_ω . We use the notation $X_n \xrightarrow[n \rightarrow \infty]{p_\nu} X$ to denote that X_n converges in probability to X as $n \rightarrow \infty$, with respect to the measure ν . That is, $X_n \xrightarrow[n \rightarrow \infty]{p_\nu} X$ means that for every $\epsilon > 0$, $\delta > 0$, we have $\nu(|X_n - X| > \epsilon) < \delta$ for all sufficiently large $n \in \mathbb{N}$. In particular, we often use the notation $\mathbb{P}_\omega(X_n \in \mathcal{A}) \xrightarrow[n \rightarrow \infty]{p_\nu} \mathbb{P}(X \in \mathcal{A})$, which is to be interpreted as meaning that, for a subset \mathcal{A} of the state space of X_n and X , we have that for every $\epsilon > 0$,

$$\int_{\omega \in \Omega} \mathbb{1}(|\mathbb{P}_\omega(X_n \in \mathcal{A}) - \mathbb{P}(X \in \mathcal{A})| > \epsilon) \nu(d\omega) \rightarrow 0 \quad \text{as } n \rightarrow \infty. \quad (5.1)$$

We prove the following conditioned versions of Theorems 3.3 and 3.4, in which $\mathcal{R}^{(n)}(\omega, \mathcal{I})$ denotes the set of ultimately recovered vertices, including the single initial infective, in an SIR epidemic (as defined in Section 2.3) on the random intersection graph $G^{(n)}$, constructed using the infectious period distribution \mathcal{I} and the sequences $(A_i, i \in \mathbb{N})$, $(B_j, j \in \mathbb{N})$ denoted by $\omega \in \Omega$.

Theorem 5.1. *For $k \in \mathbb{N}$, we have*

$$\mathbb{P}_\omega(|\mathcal{R}^{(n)}(\omega, \mathcal{I})| = k) \xrightarrow[n \rightarrow \infty]{p_\nu} \mathbb{P}(|\mathcal{Z}^f(A, B, \mathcal{I})| = k).$$

Theorem 5.2. *For every $0 < \epsilon < \rho^b(A, B, \mathcal{I})$,*

$$\mathbb{P}_\omega(|n^{-1}|\mathcal{R}^{(n)}(\omega, \mathcal{I})| - \rho^b(A, B, \mathcal{I})| < \epsilon) \xrightarrow[n \rightarrow \infty]{p_\nu} \rho(A, B, \mathcal{I}).$$

Proofs of Theorems 3.3 and 3.4. Note that, for fixed $k \in \mathbb{N}$, the sequence of random variables $(\mathbb{P}_\omega(|\mathcal{R}^{(n)}(\omega, \mathcal{I})| = k), n \in \mathbb{N})$ is uniformly integrable, so Theorem 3.3 follows immediately from Theorem 5.1 (and [18, Theorem 7.10.3]), by taking expectations with respect to the measure ν . Theorem 3.4 follows similarly from Theorem 5.2. \square

5.1 Proof of Theorem 5.1

In this proof we use three processes,

- the branching process $\mathcal{Z}^f = \mathcal{Z}^f(A, B, \mathcal{I})$,
- the branching process $\mathcal{Z}^{(n)} = \mathcal{Z}^f(A^{(n)}, B^{(n)}, \mathcal{I})$, defined similarly to $\mathcal{Z}^f(A, B, \mathcal{I})$ but with A and B replaced respectively by $A^{(n)}$ and $B^{(n)}$, defined in (2.7) and (2.8),
- the exploration process of the Epidemic Generated Graph on $G^{(n)}$, denoted by $\mathcal{R}^{(n)} = \mathcal{R}^{(n)}(\omega, \mathcal{I}) = (\mathcal{R}_0^{(n)}, \mathcal{R}_1^{(n)}, \dots)$.

In the exploration process, $\mathcal{R}_0^{(n)}$ denotes the initially infective vertex v_0 , $\mathcal{R}_1^{(n)}$ denotes the subset of vertices in $V^{(n)} \setminus \mathcal{E}_0^{(n)}$ that in the Epidemic Generated Graph have an edge to them from v_0 , $\mathcal{R}_2^{(n)}$ denotes the subset of vertices in $V^{(n)} \setminus (\mathcal{R}_0^{(n)} \cup \mathcal{R}_1^{(n)})$ that in the Epidemic Generated Graph have an edge to them from at least one member of $\mathcal{R}_1^{(n)}$, and so on. With slight abuse of notation we now use $\mathcal{R}^{(n)}$ for the exploration process, where previously it was the set of ultimately recovered vertices in $\mathcal{E}^{(n)}$. As with the branching process \mathcal{Z}^f , $|\mathcal{R}^{(n)}| = \sum_{i=0}^{\infty} |\mathcal{R}_i^{(n)}|$ is the total number of ultimately recovered vertices; note that this has precisely the same meaning as in Section 3.4.

To prove Theorem 5.1 we first show that the distribution of the total size of $\mathcal{Z}^{(n)}$ is approximately that of \mathcal{Z}^f , then that the distribution of the total size of $\mathcal{R}^{(n)}$ is approximately that of $\mathcal{Z}^{(n)}$.

Lemma 5.3. *For $k \in \mathbb{N}$, it holds that $\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k) \xrightarrow[n \rightarrow \infty]{p_\nu} \mathbb{P}(|\mathcal{Z}^f| = k)$.*

Proof. Recall that a litter in a branching process is a group of children corresponding with the number of individuals infected in a local epidemic in one clique, excluding the initial susceptible. Let the total number of (possibly empty) litters in \mathcal{Z}^f and $\mathcal{Z}^{(n)}$ be denoted by H and $H^{(n)}$, respectively. Note that if $X_n \Rightarrow X$, then $\mathcal{MP}(X_n) \Rightarrow \mathcal{MP}(X)$ [18, Theorem 7.2.19]. Recall further that $A^{(n)} \Rightarrow A$ and $B^{(n)} \Rightarrow B$ as $n \rightarrow \infty$. These latter convergence results also hold for the size-biased variants, as shown just below equation (2.1). It follows that, as $n \rightarrow \infty$, the number and sizes of litters spawned by a typical individual in $\mathcal{Z}^{(n)}$ converge in distribution to those of a corresponding typical individual in \mathcal{Z}^f . Hence, for $k \in \mathbb{N}$ and $l \in \mathbb{Z}_+$,

$$\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} = l) \xrightarrow[n \rightarrow \infty]{p_\nu} \mathbb{P}(|\mathcal{Z}^f| = k, H = l).$$

Therefore, for every $L \in \mathbb{N}$, we have

$$\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} \leq L) \xrightarrow[n \rightarrow \infty]{p_\nu} \mathbb{P}(|\mathcal{Z}^f| = k, H \leq L).$$

Note that

$$\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k) = \mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} \leq L) + \mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} > L)$$

and

$$\mathbb{P}_\omega(|\mathcal{Z}^f| = k) = \mathbb{P}_\omega(|\mathcal{Z}^f| = k, H \leq L) + \mathbb{P}_\omega(|\mathcal{Z}^f| = k, H > L).$$

Now fix $k \in \mathbb{N}$ and note that the probability of the intersection of the following events can be made arbitrarily close to 0 by making $c_1 > 0$ and $c_2 > 0$ sufficiently small and $L \in \mathbb{N}$ sufficiently large (L might depend on c_2):

- (i) $|\mathcal{Z}^f| = k$,
- (ii) $H > L$,
- (iii) the first k vertices evaluated in the branching process \mathcal{Z}^f all have infectious periods larger than c_1 , and
- (iv) at least $c_2 L$ out of the first L cliques evaluated in \mathcal{Z}^f have size ≥ 2 .

The probability that neither (iii) nor (iv) holds can also be made arbitrarily close to 0 by tuning c_1 and c_2 (recall that $\mathbb{P}(\mathcal{I} = 0) = 0$).

Combining these observations, it follows that for every $\epsilon > 0$, there exists $L \in \mathbb{N}$, such that for all $l > L$,

$$\mathbb{P}(|\mathcal{Z}^f| = k) < \mathbb{P}(|\mathcal{Z}^f| = k, H \leq l) + \epsilon/3. \quad (5.2)$$

Note that the probability that (iii) does not hold is the same for $\mathcal{Z}^{(n)}$ and \mathcal{Z}^f ; whilst given any $\delta > 0$, the fact that $\mathcal{MP}(\tilde{B}^{(n)}) \Rightarrow \mathcal{MP}(\tilde{B})$ implies that there exists $N' \in \mathbb{N}$ such that the probability that (iv) does not hold is at most $\delta/3$ for all $n \geq N'$. It then follows that for given $\epsilon > 0$, there exists $L' \in \mathbb{N}$, such that for all $l > L'$,

$$\nu\left(\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k) < \mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} \leq l) + \epsilon/3\right) > 1 - \delta/2 \quad (5.3)$$

for all sufficiently large n . Now

$$\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} \leq l) \xrightarrow[n \rightarrow \infty]{p_\nu} \mathbb{P}(|\mathcal{Z}^f| = k, H \leq l)$$

implies that for all $\epsilon > 0$ and $\delta > 0$,

$$\nu\left(\left|\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} \leq l) - \mathbb{P}(|\mathcal{Z}^f| = k, H \leq l)\right| < \epsilon/3\right) > 1 - \delta/2, \quad (5.4)$$

for all sufficiently large n . Now, using the triangle inequality,

$$\begin{aligned} \left|\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k) - \mathbb{P}(|\mathcal{Z}^f| = k)\right| &\leq \left|\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k) - \mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} \leq l)\right| \\ &\quad + \left|\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} \leq l) - \mathbb{P}(|\mathcal{Z}^f| = k, H \leq l)\right| \\ &\quad + \left|\mathbb{P}(|\mathcal{Z}^f| = k) - \mathbb{P}(|\mathcal{Z}^f| = k, H \leq l)\right|, \end{aligned}$$

whence, noting that the final term is independent of ω ,

$$\begin{aligned} \nu\left(\left|\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k) - \mathbb{P}(|\mathcal{Z}^f| = k)\right| \geq \epsilon\right) &\leq \nu\left(\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k) \geq \mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} \leq l) + \epsilon/3\right) \\ &\quad + \nu\left(\left|\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} \leq l) - \mathbb{P}(|\mathcal{Z}^f| = k, H \leq l)\right| \geq \epsilon/3\right) \\ &\quad + \mathbf{1}\left(\mathbb{P}(|\mathcal{Z}^f| = k) \geq \mathbb{P}(|\mathcal{Z}^f| = k, H \leq l) + \epsilon/3\right). \end{aligned}$$

By choosing l large enough, it follows, using (5.2), (5.3) and (5.4), that for all sufficiently large n ,

$$\nu\left(\left|\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k) - \mathbb{P}(|\mathcal{Z}^f| = k)\right| \geq \epsilon\right) \leq \delta/2 + \delta/2 + 0 = \delta$$

and the lemma then follows. \square

Lemma 5.4. For $k \in \mathbb{N}$, $\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| \leq k) - \mathbb{P}_\omega(|\mathcal{R}^{(n)}| \leq k) \xrightarrow[n \rightarrow \infty]{p_\nu} 0$.

Proof. The proof follows from a standard coupling argument, described below. Firstly though, for each $n \in \mathbb{N}$, let $v_0^{(n)}$ be a vertex chosen uniformly at random from $V^{(n)}$ and let $v_1^{(n)}, v_2^{(n)}, \dots$ be independently chosen vertices from $V^{(n)}$, where the probability that a given vertex is chosen is proportional to its A -weight. Let $a_0^{(n)}, a_1^{(n)}, \dots$ be the respective A -weights of $v_0^{(n)}, v_1^{(n)}, \dots$. Let $\mathcal{I}_0^{(n)}$ be the type assigned to vertex $v_0^{(n)}$. Let $v'_1{}^{(n)}, v'_2{}^{(n)}, \dots$ be independently chosen vertices (representing cliques) from $V'^{(n)}$ where the probability that a given vertex is chosen is proportional to its B -weight. The B -weights of $v'_1{}^{(n)}, v'_2{}^{(n)}, \dots$ are denoted by $b_1^{(n)}, b_2^{(n)}, \dots$, respectively. Let the random variable

$$T^{(n)} = \min(i \in \mathbb{N} : v_i^{(n)} = v_j^{(n)} \text{ for some } j < i)$$

be the smallest index at which a vertex from $V^{(n)}$ is chosen a second time. Similarly, define

$$T'^{(n)} = \min(i \in \mathbb{N} : v'_i{}^{(n)} = v'_j{}^{(n)} \text{ for some } j < i).$$

The constructions of $\mathcal{Z}^{(n)}$ and $\mathcal{R}^{(n)}$ are coupled as follows. The ancestor of $\mathcal{Z}^{(n)}$ spawns a $\mathcal{P}(a_0^{(n)})$ number of (possibly empty) litters, l' say. The cliques that the initial infective in $\mathcal{R}^{(n)}$ belongs to are given by $v_1^{(n)}, v_2^{(n)}, \dots, v_{l'}^{(n)}$, which might contain duplicates; the B -weights associated with these litters are $b_1^{(n)}, b_2^{(n)}, \dots, b_{l'}^{(n)}$. If $T^{(n)} > l'$, then there are no duplicates amongst $v_1^{(n)}, v_2^{(n)}, \dots, v_{l'}^{(n)}$ and the processes stay coupled. If not, the construction can be continued but the details are not important for our purposes.

If the coupling continues the sizes of the litters (recall that litters are defined both for the epidemic process and the branching process) are then determined. For each $i = 1, 2, \dots, l'$, the size of litter i is distributed as the number of initially susceptible individuals which are ultimately infected by a local epidemic in a group with one initially infectious individual, having infectious period $\mathcal{I}_0^{(n)}$, and a $\mathcal{P}(b_i^{(n)})$ distributed number of initially susceptible individuals. The litter sizes are all independent. Say that the total number of vertices in the l' litters is l , then they get A -weights $a_1^{(n)}, a_2^{(n)}, \dots, a_l^{(n)}$ and types $\mathcal{I}_1^{(n)}, \mathcal{I}_2^{(n)}, \dots, \mathcal{I}_l^{(n)}$, which are i.i.d. and distributed as \mathcal{I} . If $l < T^{(n)}$ the coupling continues and the generation 1 vertices are $v_1^{(n)}, v_2^{(n)}, \dots, v_l^{(n)}$. The coupling now proceeds in the obvious way. Note that in this construction we have not yet decided which vertices are in the same clique (of the random intersection graph) as $v_1^{(n)}$ but are not infected by the local epidemic.

Let $H^{(n)}$ be as in the proof of Lemma 5.3 and let $H^{(*n)}$ be the corresponding number for $\mathcal{R}^{(n)}$. We need to prove that for $k \in \mathbb{N}$ and $l \in \mathbb{Z}_+$,

$$\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} = l) - \mathbb{P}_\omega(|\mathcal{R}^{(n)}| = k, H^{(*n)} = l) \xrightarrow[n \rightarrow \infty]{p_\nu} 0,$$

and then deduce the statement of the lemma as in the latter part of the proof of Lemma 5.3. Note that the coupling gives

$$\begin{aligned} \mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} = l, T^{(n)} > k, T'^{(n)} > l) \\ = \mathbb{P}_\omega(|\mathcal{R}^{(n)}| = k, H^{(*n)} = l, T^{(n)} > k, T'^{(n)} > l). \end{aligned} \quad (5.5)$$

Furthermore, letting $C^{(n)}(k, l) = \{T^{(n)} \leq k\} \cup \{T'^{(n)} \leq l\}$, we have

$$\begin{aligned} \mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} = l) &= \mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} = l, T^{(n)} > k, T'^{(n)} > l) \\ &\quad + \mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} = l, C^{(n)}(k, l)). \end{aligned}$$

Note that the second term on the right hand side of this expression is bounded above by $\mathbb{P}_\omega(C^{(n)}(k, l))$.

Recall from Section 2.2 that $\mu = \mathbb{E}[A] = \alpha \mathbb{E}[B] < \infty$, which implies that the total weight of vertices in $V^{(n)}$ with weight exceeding $\log n$ is ν -almost surely $o(n)$. (To show this, note that, since $\mu < \infty$, for any $N > 0$,

$$n^{-1} \sum_{i=1}^n A_i \mathbb{1}(A_i > N) \xrightarrow{a.s.} \mathbb{E}[A \mathbb{1}(A > N)] \quad \text{as } n \rightarrow \infty$$

and $\mathbb{E}[A \mathbb{1}(A > N)] \rightarrow 0$ as $N \rightarrow \infty$.) A similar result holds for the weights of the vertices in $V'^{(n)}$. Hence, for every $k, l \in \mathbb{N}$, the probability that both $\max(a_i^{(n)} : 0 \leq i \leq k) \leq \log n$ and $\max(b_j^{(n)} : 1 \leq j \leq l) \leq \log n$ converges to 1 as $n \rightarrow \infty$. Thus, the total weight of

the first k vertices and the first l litters chosen in the branching process is ν -almost surely $O(\log n)$. By a birthday problem argument we deduce that $\mathbb{P}_\omega(C^{(n)}(l, k)) \xrightarrow[n \rightarrow \infty]{p_\nu} 0$. (Note that if $M_n(k)$ is the number of distinct pairs (i, j) with $0 \leq i < j \leq k$ and $v_i^{(n)} = v_j^{(n)}$, then under the above restrictions, $\mathbb{E}_\omega[M_n(k)] \leq \frac{k(k-1)}{2} \frac{\log n}{L^{(n)}} \xrightarrow[n \rightarrow \infty]{p_\nu} 0$). Thus, for every $k, l \in \mathbb{N}$,

$$\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} = l) - \mathbb{P}_\omega(|\mathcal{Z}^{(n)}| = k, H^{(n)} = l, T^{(n)} > k, T'^{(n)} > l) \xrightarrow[n \rightarrow \infty]{p_\nu} 0.$$

Similarly, we deduce that, again for all $k, l \in \mathbb{N}$,

$$\mathbb{P}_\omega(|\mathcal{R}^{(n)}| = k, H^{(*n)} = l) - \mathbb{P}_\omega(|\mathcal{R}^{(n)}| = k, H^{(*n)} = l, T^{(n)} > k, T'^{(n)} > l) \xrightarrow[n \rightarrow \infty]{p_\nu} 0;$$

which, together with (5.5), yields the lemma. \square

Theorem 5.1 follows immediately by combining Lemmas 5.3 and 5.4.

5.2 Proof of Theorem 5.2

Before considering susceptibility sets and backward branching processes, we prove the following extension of Lemma 5.3 which is required later in this section.

Lemma 5.5. $\rho(A^{(n)}, B^{(n)}, \mathcal{I}) \xrightarrow[n \rightarrow \infty]{p_\nu} \rho(A, B, \mathcal{I})$.

Proof. For every $k \in \mathbb{Z}_+$, define the random variable

$$\mathcal{I}^k(\mathcal{I}) = \begin{cases} 2^{-k} \lfloor 2^k \mathcal{I} \rfloor & \text{if } \mathcal{I} < 2^k, \\ 2^k & \text{if } \mathcal{I} \in [2^k, \infty), \\ \infty & \text{if } \mathcal{I} = \infty. \end{cases}$$

That is, \mathcal{I}^k is a random variable which can take only finitely many values and for $j = 1, 2, \dots, 4^k - 1$,

$$\mathbb{P}(\mathcal{I}^k = j2^{-k}) = \mathbb{P}(\mathcal{I} \in [j2^{-k}, (j+1)2^{-k})),$$

while $\mathbb{P}(\mathcal{I}^k = 2^k) = \mathbb{P}(\mathcal{I} \in [2^k, \infty))$ and $\mathbb{P}(\mathcal{I}^k = \infty) = \mathbb{P}(\mathcal{I} = \infty)$. It is clear that $\mathcal{I}^k \Rightarrow \mathcal{I}$ as $k \rightarrow \infty$ and that \mathcal{I}^k is stochastically smaller than \mathcal{I}^{k+1} for all $k \in \mathbb{Z}_+$.

For non-negative random variables X and Y , the function $\tilde{\rho}(X, Y, \mathcal{I}^k)$ is pointwise non-decreasing in k , since it is the survival probability of a branching process and (stochastically) increasing the distribution of the infectious periods, and thus also of the offspring distribution, cannot decrease the survival probability of the process. By monotonicity we have that $\lim_{k \rightarrow \infty} \tilde{\rho}(X, Y, \mathcal{I}^k)$ exists pointwise, and by the monotone convergence theorem this limit satisfies (4.3) for $\tilde{\rho}(X, Y, \mathcal{I})$. By Lemma 5.3 we know that for every $k \in \mathbb{N}$, $\mathbb{P}_\omega(|\mathcal{Z}^{(n)}| > k) \xrightarrow[n \rightarrow \infty]{p_\nu} \mathbb{P}(|\mathcal{Z}^f| > k)$. This implies that for every $\epsilon > 0$ and $\delta > 0$, there exists $N_0 \in \mathbb{N}$ such that for $n > N_0$, we have

$$\nu(\rho(A^{(n)}, B^{(n)}, \mathcal{I}) < \rho(A, B, \mathcal{I}) + \epsilon) > 1 - \delta/2. \quad (5.6)$$

Furthermore, for every $\epsilon > 0$, there exists $K \in \mathbb{N}$ such that for $k > K$, we have

$$\rho(A, B, \mathcal{I}^k) > \rho(A, B, \mathcal{I}) - \epsilon/2.$$

Similarly, for every $\epsilon > 0$, $\delta > 0$ and $k \in \mathbb{N}$, there exist $N_k \in \mathbb{N}$ such that for $n > N_k$, we have

$$\nu(\rho(A^{(n)}, B^{(n)}, \mathcal{I}^k) > \rho(A, B, \mathcal{I}^k) - \epsilon/2) > 1 - \delta/2,$$

while for every $k \in \mathbb{N}$ (and $\omega \in \Omega$), $\rho(A^{(n)}, B^{(n)}, \mathcal{I}) \geq \rho(A^{(n)}, B^{(n)}, \mathcal{I}^k)$. Combining these statements establishes that, for every $\epsilon > 0$ and $\delta > 0$, there exists $N \in \mathbb{N}$ such that for all $n > N$, we have

$$\nu(\rho(A^{(n)}, B^{(n)}, \mathcal{I}) > \rho(A, B, \mathcal{I}) - \epsilon) > 1 - \delta/2.$$

Combining this with (5.6) completes the proof of the lemma. \square

In order to prove Theorem 5.2, we investigate the susceptibility sets of two uniformly at random chosen vertices in the subgraph $\hat{G}^{(n)}$ (of $G^{(n)}$), which is defined as follows. Let $\hat{\mathbb{A}}^{(n)}$ be constructed from $\mathbb{A}^{(n)}$ by ignoring all vertices in $V^{(n)}$ and $V'^{(n)}$ that have weights larger than $\log n$ and ignoring all edges that are incident to such vertices. The graph $\hat{G}^{(n)}$ is constructed from $\hat{\mathbb{A}}^{(n)}$ in the same way that $G^{(n)}$ is constructed from $\mathbb{A}^{(n)}$.

We can create a realisation of $\hat{\mathbb{A}}^{(n)}$ as follows. Define the vertex sets $\hat{V}^{(n)} = (v_i \in V^{(n)} : A_i \leq \log n)$ and $\hat{V}'^{(n)} = (v'_j \in V'^{(n)} : B_j \leq \log n)$. Conditional upon the weights of the vertices in $\mathbb{A}^{(n)}$, (i) vertices $v_i \in \hat{V}^{(n)}$ and $v'_j \in \hat{V}'^{(n)}$ share in $\hat{\mathbb{A}}^{(n)}$ a $\mathcal{P}(A_i B_j / (\mu n))$ number of edges and (ii) the number of edges between distinct pairs of vertices are independent. Let

$$\hat{L}^{(n)} = \sum_{i: v_i \in \hat{V}^{(n)}} A_i \quad \text{and} \quad (5.7)$$

$$\hat{L}'^{(n)} = \sum_{j: v'_j \in \hat{V}'^{(n)}} B_j. \quad (5.8)$$

Then the degree of vertex $v_i \in \hat{V}^{(n)}$ in $\hat{\mathbb{A}}^{(n)}$ is $\mathcal{P}(A_i \hat{L}'^{(n)} / (\mu n))$ and the degree of $v'_j \in \hat{V}'^{(n)}$ is $\mathcal{P}(B_j \hat{L}^{(n)} / (\mu n))$. We construct from $\hat{\mathbb{A}}^{(n)}$ an identically distributed copy of $\mathbb{A}^{(n)}$ by adding the vertices from $V^{(n)} \setminus \hat{V}^{(n)}$ and $V'^{(n)} \setminus \hat{V}'^{(n)}$ and, if $v_i \in V^{(n)}$ and $v'_j \in V'^{(n)}$ are not both in $\hat{\mathbb{A}}^{(n)}$, letting v_i and v'_j share a $\mathcal{P}(A_i B_j / (\mu n))$ number of newly-added edges, independently of the number of edges between other vertices.

We compute the probability that the susceptibility sets of two vertices in $\hat{G}^{(n)}$ survive until at least generation

$$t_n = \lceil \log \log n \rceil. \quad (5.9)$$

(Note that, as $n \rightarrow \infty$, if it survives, the total number of individuals in the branching process $\mathcal{Z}^b(A, B, \mathcal{I})$ in generations $0, 1, \dots, t_n$ is of order $O(\log n)$ and a standard coupling argument, similar to that in the proof of Lemma 5.4, shows that, with probability tending to 1 as $n \rightarrow \infty$, a susceptibility set process and its approximating branching process coincide over generations $0, 1, \dots, t_n$. Thus for large n , if the susceptibility set process survives until generation t_n , its size will then be of order $O(\log n)$; cf. the discussion in Section 3.3.)

Next, we show that, given any $\epsilon > 0$, there exists $K \in \mathbb{N}$ such that the probability that the t_n -th generation of an individual's susceptibility set is empty on $\hat{G}^{(n)}$ and the total size of its susceptibility set on $G^{(n)}$ exceeds K is less than ϵ for all sufficiently large n ; see Lemma 5.10. We then explore the forward process in $G^{(n)}$, where we ignore the vertices and cliques already explored in the two backward processes. We show that if the epidemic

size is not $\Theta(1)$, then, with probability tending to 1 as $n \rightarrow \infty$, it is $\Theta(n)$. After this we attempt to connect the forward process with the generation t_n vertices of the backward processes and show that, in the event of a large outbreak, the probability that at least 1 of the vertices in generation t_n of a susceptibility set (if this generation is not empty) is ultimately recovered converges to 1 as $n \rightarrow \infty$.

We construct a coupling of two independent branching processes and the susceptibility sets of v_1 and v_2 in $\hat{G}^{(n)}$ (which by exchangeability is equivalent to choosing two distinct vertices uniformly at random), assuming that $A_1, A_2 \leq \log n$. We therefore define (cf. equations (2.5)–(2.8)) $\hat{A}_i^{(n)} = A_i \mathbf{1}(A_i \leq \log n) \hat{L}^{(n)} / (\mu n)$ and $\hat{B}_i^{(n)} = B_i \mathbf{1}(B_i \leq \log n) \hat{L}^{(n)} / (\mu n)$; and let $\hat{c}_A^{(n)} = \sum_{i=1}^n \mathbf{1}(A_i \leq \log n)$ and $\hat{c}_B^{(n)} = \sum_{i=1}^{\lfloor \alpha n \rfloor} \mathbf{1}(B_i \leq \log n)$. The random variables $\hat{A}^{(n)}$ and $\hat{B}^{(n)}$ are defined by

$$\begin{aligned} \mathbb{P}_\omega(\hat{A}^{(n)} \leq x) &= |\{1 \leq i \leq \hat{c}_A^{(n)} : \hat{A}_i^{(n)} \leq x\}| / \hat{c}_A^{(n)} \quad (x \geq 0) \quad \text{and} \\ \mathbb{P}_\omega(\hat{B}^{(n)} \leq x) &= |\{1 \leq i \leq \hat{c}_B^{(n)} : \hat{B}_i^{(n)} \leq x\}| / \hat{c}_B^{(n)} \quad (x \geq 0). \end{aligned}$$

The processes through which the construction of the susceptibility set of v_i ($i \in \{1, 2\}$) takes place are denoted by

$$\hat{\mathcal{S}}^i = \hat{\mathcal{S}}^i(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I}) = (\hat{\mathcal{S}}_j^i, j \in \mathbb{Z}_+).$$

The two independent branching processes are $\mathcal{Z}^{b,i} = \mathcal{Z}^{b,i}(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})$, for $i \in \{1, 2\}$, where $\hat{A}^{(n)}$ and $\hat{B}^{(n)}$ are as above. The corresponding susceptibility set processes in $G^{(n)}$ are denoted by \mathcal{S}^i for $i \in \{1, 2\}$. When no confusion is possible, we sometimes suppress the reference to the starting vertex i .

We use the following lemmas.

Lemma 5.6. *Let $0 < \epsilon < 3/e - 1$. For $k \in \mathbb{N}$, let $(X_i(k), i \in \mathbb{N})$ be a sequence of i.i.d. $\mathcal{P}((1 + \epsilon) \log k)$ random variables. Then, for every $C > 0$,*

$$\mathbb{P}(\max_{1 \leq i \leq \lfloor Ck \rfloor} X_i(k) \leq 3 \log k) \rightarrow 1 \quad \text{as } k \rightarrow \infty.$$

Proof. Since $e^k = \sum_{i=0}^{\infty} k^i / i!$, we have $k! > k^k e^{-k}$. Then

$$\begin{aligned} \mathbb{P}(X_1(k) > 3 \log k) &= \sum_{j=\lceil 3 \log k \rceil}^{\infty} \frac{((1 + \epsilon) \log k)^j}{j!} \frac{1}{k^{1+\epsilon}} \\ &\leq \frac{1}{k^{1+\epsilon}} \sum_{j=\lceil 3 \log k \rceil}^{\infty} \frac{((1 + \epsilon) \log k)^j}{j^j e^{-j}} \\ &< \frac{1}{k^{1+\epsilon}} \sum_{j=\lceil 3 \log k \rceil}^{\infty} ((1 + \epsilon)e/3)^j \\ &< \frac{3}{3 - (1 + \epsilon)e} k^{-1-\epsilon+3(1+\log[1+\epsilon]-\log 3)}. \end{aligned}$$

The probability that none out of $\lfloor Ck \rfloor$ independent copies of $X_1(k)$ exceeds $3 \log k$ is thus

given by

$$\begin{aligned}
(1 - \mathbb{P}(X_1(k) > 3 \log k))^{\lfloor Ck \rfloor} &> \left(1 - \frac{3}{3 - (1 + \epsilon)e} k^{-1 - \epsilon + 3(1 + \log[1 + \epsilon] - \log 3)}\right)^{Ck} \\
&> 1 - Ck \frac{3}{3 - (1 + \epsilon)e} k^{-1 - \epsilon + 3(1 + \log[1 + \epsilon] - \log 3)} \\
&= 1 - \frac{3C}{3 - (1 - \epsilon)e} k^{3(1 + \log[1 + \epsilon] - \log 3) - \epsilon},
\end{aligned}$$

which converges to 1 as $k \rightarrow \infty$, since $0 < \epsilon < 3/e - 1$. \square

Recall that the distance between two vertices in a graph is the number of edges in the shortest path connecting those vertices.

Lemma 5.7. *For ν -almost all $\omega \in \Omega$, the probability that the total number and the total weight of vertices within distance $2t_n$ of the set $\{v_1, v_2\}$ in $\hat{\mathbb{A}}^{(n)}$ are both smaller than $n^{1/3}$ converges to 1 as $n \rightarrow \infty$.*

Proof. All vertices in $\hat{\mathbb{A}}^{(n)}$ have weight at most $\log n$, so their degrees in $\hat{\mathbb{A}}^{(n)}$ are stochastically dominated by i.i.d. $\mathcal{P}(\log n \max(\hat{L}^{(n)}, \hat{L}'^{(n)})/(\mu n))$ random variables. For every $\epsilon > 0$, we have by the strong law of large numbers that $\mathbf{1}(\max(\hat{L}^{(n)}, \hat{L}'^{(n)})/(\mu n) < 1 + \epsilon) \xrightarrow{a.s.} 1$ as $n \rightarrow \infty$. We know by Lemma 5.6 that, with probability tending to 1 as $n \rightarrow \infty$, none of the at most $n + \lfloor \alpha n \rfloor$ vertices in $\hat{\mathbb{A}}^{(n)}$ has degree exceeding $3 \log n$. So, using a straightforward branching process approximation, the number of vertices within graph distance $2t_n$ of v_1 and v_2 is, with probability tending to 1 as $n \rightarrow \infty$, bounded above by

$$2 \sum_{k=1}^{2t_n} (3 \log n)^k = O((3 \log n)^{2t_n+1}).$$

Since $2t_n + 1 = 2\lceil \log \log n \rceil + 1 < 2 \log \log n + 3$, we have

$$\begin{aligned}
(3 \log n)^{2t_n+1} &< (3 \log n)^{3+2 \log \log n} \\
&= (3 \log n)^3 e^{2 \log \log n (\log 3 + \log \log n)} = o(n^{1/3} / \log n),
\end{aligned}$$

so the total weight of the vertices is $o(n^{1/3})$. \square

For $i \in \{1, 2\}$, let $K^i(t_n)$ be the set of vertices in $V^{(n)}$ within distance $2t_n$ of v_i in $\hat{\mathbb{A}}^{(n)}$, and let $K'^i(t_n)$ be the set of vertices in $V'^{(n)}$ within distance $2t_n$ of v_i in $\hat{\mathbb{A}}^{(n)}$. Lemma 5.7 implies that, with probability tending to 1 as $n \rightarrow \infty$, none of the sets $K^1(t_n)$, $K^2(t_n)$, $K'^1(t_n)$ and $K'^2(t_n)$ has total vertex or clique weight exceeding $n^{1/3}$. Furthermore, with probability tending to 1 as $n \rightarrow \infty$, the total number of vertices in $K^1(t_n)$ is less than $n^{1/3}$. Conditioned on $K^2(t_n)$ having total weight less than $n^{1/3}$ and $K^1(t_n)$ containing less than $n^{1/3}$ vertices, the probability that $K^1(t_n)$ and $K^2(t_n)$ share an edge is bounded above by $1 - (1 - n^{1/3}/\hat{L}_n)^{n^{1/3}} < n^{2/3}/\hat{L}_n$, which converges ν -almost surely to 0 as $n \rightarrow \infty$. So, for ν -almost all $\omega \in \Omega$, the \mathbb{P}_ω -probability that K^1 and K^2 share a vertex converges to 0 as $n \rightarrow \infty$. Similarly, we deduce that for ν -almost all $\omega \in \Omega$, the \mathbb{P}_ω -probability that K'^1 and K'^2 share a clique converges to 0 as $n \rightarrow \infty$.

Recall the definition of R_* from (3.1) and write R_* as $R_*(A, B, \mathcal{I})$ to show explicitly its dependence on the distributions of A, B and \mathcal{I} .

Lemma 5.8. *For $0 < c < \log R_*$, it holds that*

$$\mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}^i| > (\log n)^c \mid |\hat{\mathcal{S}}_{t_n}^i| > 0) \xrightarrow[n \rightarrow \infty]{p_\nu} 1.$$

Proof. By Lemma 5.7 and standard coupling arguments, similar to those used in the proof of Lemma 5.4, we can replace $\hat{\mathcal{S}}$ by the branching process $\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})$.

For $n \in \mathbb{N}$, let $\hat{A}_*^{(n)}$ be a random variable having distribution function given by

$$\mathbb{P}_\omega(\hat{A}_*^{(n)} \leq x) = \sup_{i \geq n} \mathbb{P}_\omega(\hat{A}^{(i)} \leq x) \quad (x \in \mathbb{R})$$

and define $\hat{B}_*^{(n)}$ similarly. Observe that $\hat{A}_*^{(n)} \Rightarrow A$ and $\hat{B}_*^{(n)} \Rightarrow B$ as $n \rightarrow \infty$. Furthermore, for all $n \in \mathbb{N}$, $\hat{A}_*^{(n)}$ (respectively, $\hat{B}_*^{(n)}$) is stochastically dominated by $\hat{A}_*^{(n+1)}$ (respectively, $\hat{B}_*^{(n+1)}$). Therefore $R_*(\hat{A}_*^{(n)}, \hat{B}_*^{(n)}, \mathcal{I})$ is also stochastically increasing in n . By the Skorokhod representation theorem [18, Theorem 7.2.14] and the monotone convergence theorem we have that

$$R_*(\hat{A}_*^{(n)}, \hat{B}_*^{(n)}, \mathcal{I}) \xrightarrow[n \rightarrow \infty]{p_\nu} R_*(A, B, \mathcal{I}).$$

In particular, there exists $N = N(\omega)$ such that $R_*(\hat{A}_*^{(n)}, \hat{B}_*^{(n)}, \mathcal{I}) > e^c$, for every $n > N$. So, by [20, Theorem 2.7.1] it follows that

$$\mathbb{P}_\omega(|\mathcal{Z}_{t_n}^b(\hat{A}_*^{(n)}, \hat{B}_*^{(n)}, \mathcal{I})| > (\log n)^c) - \mathbb{P}_\omega(|\mathcal{Z}_{t_n}^b(\hat{A}_*^{(n)}, \hat{B}_*^{(n)}, \mathcal{I})| > 0) \xrightarrow[n \rightarrow \infty]{p_\nu} 0.$$

The second probability in this expression converges to $\rho^b(A, B, \mathcal{I})$ by [12, Lemma 4.1] and the lemma then follows by observing that $|\mathcal{Z}_{t_n}^b(\hat{A}_*^{(n)}, \hat{B}_*^{(n)}, \mathcal{I})|$ is stochastically smaller than $|\mathcal{Z}_{t_n}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})|$. \square

Up to now, we have investigated the behavior of the susceptibility sets of vertices in $\hat{G}^{(n)}$. This is only an intermediate step before analyzing susceptibility sets in $G^{(n)}$. To make the connection between the two graphs we use the following two lemmas.

Lemma 5.9. *For $k \in \mathbb{N}$,*

$$\mathbb{P}_\omega(|\hat{\mathcal{S}}(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| = k) - \mathbb{P}_\omega(|\mathcal{S}(A^{(n)}, B^{(n)}, \mathcal{I})| = k) \xrightarrow[n \rightarrow \infty]{p_\nu} 0.$$

Proof. In order to simplify the notation we suppress the explicit dependence on $\hat{A}^{(n)}, \hat{B}^{(n)}$ and \mathcal{I} . We denote by \mathcal{S}^i the set of cliques containing vertices in the susceptibility set \mathcal{S}^i . We prove that

$$\mathbb{P}_\omega(|\hat{\mathcal{S}}| = k, |\hat{\mathcal{S}}'| = l) - \mathbb{P}_\omega(|\mathcal{S}| = k, |\mathcal{S}'| = l) \xrightarrow[n \rightarrow \infty]{p_\nu} 0, \quad (5.10)$$

from which the lemma follows using similar arguments to those in the proof of Lemma 5.3, which are not repeated here.

Recall that we can construct $G^{(n)}$ from $\hat{G}^{(n)}$, by considering the vertices in $V^{(n)} \setminus \hat{V}^{(n)}$ and $V'^{(n)} \setminus \hat{V}'^{(n)}$ and then connecting them in the usual way with each other and with vertices in $V^{(n)}$ and $V'^{(n)}$ to obtain $\mathbb{A}^{(n)}$. As in the proof of Lemma 5.4, $\mu < \infty$ implies that

$$\sum_{i=1}^n A_i \mathbb{1}(A_i > \log[n]) = L^{(n)} - \hat{L}^{(n)} = o(n) \quad \nu\text{-almost surely.}$$

Therefore,

$$\frac{L^{(n)} - \hat{L}^{(n)}}{L^{(n)}} \xrightarrow{a.s.} 0 \quad \text{as } n \rightarrow \infty.$$

This implies that $1 - \hat{L}^{(n)}/L^{(n)}$ converges in probability to 0. In particular there is an increasing sequence of natural numbers $(p_i, i \in \mathbb{N})$, such that for all $n > p_i$, we have $\nu(1 - \hat{L}^{(n)}/L^{(n)} < 4^{-i}) > 1 - 2^{-i}$. Define the function $\xi : \mathbb{N} \rightarrow \mathbb{N}$ by $\xi(n) = 2^i$ if $p_i \leq n < p_{i+1}$. This function increases to infinity and

$$\mathbb{1}\left(L^{(n)} - \hat{L}^{(n)} < (\xi(n))^{-1} L^{(n)}\right) \xrightarrow[n \rightarrow \infty]{p_\nu} 1. \quad (5.11)$$

Similarly, there exists a function $\xi'(n)$ which increases to ∞ , such that

$$\mathbb{1}\left(L'^{(n)} - \hat{L}'^{(n)} < (\xi'(n))^{-1} L'^{(n)}\right) \xrightarrow[n \rightarrow \infty]{p_\nu} 1. \quad (5.12)$$

Let $\hat{L}_{(k)}^{(n)}$ (respectively, $\hat{L}'_{(k)}^{(n)}$) be the weight of the first k vertices from $\hat{V}^{(n)}$ (respectively, $\hat{V}'^{(n)}$) explored in $\hat{\mathcal{S}}$. Note that

$$\mathbb{P}_\omega\left(|\hat{\mathcal{S}}| = k, |\hat{\mathcal{S}}'| = l \mid \hat{L}_{(k)}^{(n)} \geq (\xi'(n))^{1/2} \cup \hat{L}'_{(l)}^{(n)} \geq (\xi(n))^{1/2}\right) \xrightarrow[n \rightarrow \infty]{p_\nu} 0,$$

since if the conditioning event occurs then the probability that the susceptibility set does not extend further goes to 0 as $n \rightarrow \infty$. It follows that

$$\mathbb{P}_\omega\left(|\hat{\mathcal{S}}| = k, |\hat{\mathcal{S}}'| = l, \hat{L}_{(k)}^{(n)} < (\xi'(n))^{1/2}, \hat{L}'_{(l)}^{(n)} < (\xi(n))^{1/2}\right) - \mathbb{P}_\omega(|\hat{\mathcal{S}}| = k, |\hat{\mathcal{S}}'| = l) \xrightarrow[n \rightarrow \infty]{p_\nu} 0. \quad (5.13)$$

Given ω , when constructing the graph $G^{(n)}$ from $\hat{G}^{(n)}$, the expected number of newly-added edges between the first k vertices from $\hat{V}^{(n)}$ explored in $\hat{\mathcal{S}}$ and $V^{(n)} \setminus \hat{V}^{(n)}$ is

$$F_k^{(n)} = \frac{\hat{L}_{(k)}^{(n)}(L^{(n)} - \hat{L}^{(n)})}{\mu n}.$$

Suppose that $\hat{L}_{(k)}^{(n)} < (\xi'(n))^{1/2}$. Then

$$F_k^{(n)} \leq (\xi'(n))^{1/2} \frac{(L^{(n)} - \hat{L}^{(n)})}{L^{(n)}} \frac{L^{(n)}}{n\mu},$$

which, together with (5.12) and the fact that $L^{(n)}/(n\mu) \xrightarrow{a.s.} 1$ as $n \rightarrow \infty$, yields

$$F_k^{(n)} \mathbb{1}(\hat{L}_{(k)}^{(n)} < (\xi'(n))^{1/2}) \xrightarrow[n \rightarrow \infty]{p_\nu} 0.$$

Combining this, and a corresponding result for the number of newly-added edges between the first l vertices from $\hat{V}'^{(n)}$ explored in $\hat{\mathcal{S}}$ and $V^{(n)} \setminus \hat{V}^{(n)}$, with (5.13) establishes that

$$\mathbb{P}_\omega\left(|\hat{\mathcal{S}}| = k, |\hat{\mathcal{S}}'| = l, \mathcal{S} \cap (V^{(n)} \setminus \hat{V}^{(n)}) \neq \emptyset, \mathcal{S}' \cap (V'^{(n)} \setminus \hat{V}'^{(n)}) \neq \emptyset\right) \xrightarrow[n \rightarrow \infty]{p_\nu} 0,$$

which completes the proof of (5.10) and thus of the lemma. \square

Lemma 5.10. *For every $\epsilon > 0$ there exists $K \in \mathbb{N}$ such that*

$$\mathbb{1}(\mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| = 0, |\mathcal{S}(A^{(n)}, B^{(n)}, \mathcal{I})| > K) < \epsilon) \xrightarrow[n \rightarrow \infty]{p_\nu} 1.$$

Proof. For ease of presentation we suppress the dependence on the distributions of the weights and infectious periods, writing $\hat{\mathcal{S}}$ for $\hat{\mathcal{S}}(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})$ and \mathcal{S} for $\mathcal{S}(A^{(n)}, B^{(n)}, \mathcal{I})$. First note that, as in the proof of Lemma 5.8, we can use branching process approximations to show that for every $K \in \mathbb{N}$ we have

$$\mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}| = 0, |\hat{\mathcal{S}}| > K) - \mathbb{P}_\omega(|\mathcal{Z}_{t_n}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| = 0, |\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| > K) \xrightarrow[n \rightarrow \infty]{p_\nu} 0. \quad (5.14)$$

Now,

$$\begin{aligned} & \mathbb{P}_\omega(|\mathcal{Z}_{t_n}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| = 0, |\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| > K) \\ &= \mathbb{P}_\omega(|\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| > K) \\ &\quad - \mathbb{P}_\omega(|\mathcal{Z}_{t_n}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| > 0, |\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| > K) \\ &= \mathbb{P}_\omega(|\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| > K) - \mathbb{P}_\omega(|\mathcal{Z}_{t_n}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| > 0), \end{aligned} \quad (5.15)$$

for all sufficiently large n , since $|\mathcal{Z}_{t_n}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| > 0$ implies that $|\mathcal{Z}^b(A^{(n)}, B^{(n)}, \mathcal{I})| > t_n$. Arguing as in the proof of Lemma 5.3 shows that

$$\mathbb{P}_\omega(|\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| > K) \xrightarrow[n \rightarrow \infty]{p_\nu} \mathbb{P}_\omega(|\mathcal{Z}^b(A, B, \mathcal{I})| > K). \quad (5.16)$$

To deal with the second term on the right hand side of (5.15), observe that

$$\begin{aligned} & \mathbb{P}_\omega(|\mathcal{Z}_{t_n}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| > 0) \\ &= \mathbb{P}_\omega(|\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| = \infty) \\ &\quad + \mathbb{P}_\omega(|\mathcal{Z}_{t_n}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| > 0, |\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| < \infty) \\ &\leq \mathbb{P}_\omega(|\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| = \infty) + \mathbb{P}_\omega(|\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| \in (t_n, \infty)). \end{aligned} \quad (5.17)$$

Now, given any $\epsilon > 0$, there exists $L \in \mathbb{N}$ such that $\mathbb{P}(|\mathcal{Z}^b(A, B, \mathcal{I})| \in (L, \infty)) < \epsilon$. (If $R_* \leq 1$ then $|\mathcal{Z}^b|$ is almost surely finite and the statement follows immediately. If $R_* > 1$, the statement follows by writing $\mathbb{P}(|\mathcal{Z}^b| \in (L, \infty)) = \rho^b \mathbb{P}(|\mathcal{Z}^b| \in (L, \infty) | |\mathcal{Z}^b| < \infty)$ and using the fact that a supercritical Galton-Watson process conditioned on extinction is probabilistically equivalent to an associated subcritical Galton-Watson process [13].) Further, (5.16) and [12, Lemma 4.1] imply that

$$\mathbb{P}_\omega(|\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| \in (L, \infty)) \xrightarrow[n \rightarrow \infty]{p_\nu} \mathbb{P}(|\mathcal{Z}^b(A, B, \mathcal{I})| \in (L, \infty)),$$

so

$$\mathbb{1}(\mathbb{P}_\omega(|\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| \in (L, \infty)) < \epsilon) \xrightarrow[n \rightarrow \infty]{p_\nu} 1,$$

which implies that

$$\mathbb{1}(\mathbb{P}_\omega(|\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| \in (t_n, \infty)) < \epsilon) \xrightarrow[n \rightarrow \infty]{p_\nu} 1.$$

As this holds for any $\epsilon > 0$, it follows from (5.15), (5.16) and (5.17), with another application of [12, Lemma 4.1], that

$$\begin{aligned} \mathbb{P}_\omega(|\mathcal{Z}_{t_n}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| = 0, |\mathcal{Z}^b(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I})| > K) \\ \xrightarrow[n \rightarrow \infty]{p_\nu} \mathbb{P}(|\mathcal{Z}^b(A, B, \mathcal{I})| \in (K, \infty)). \end{aligned} \quad (5.18)$$

Now $\mathbb{P}(|\mathcal{Z}^b(A, B, \mathcal{I})| \in (K, \infty))$ can be made arbitrarily close to 0 by choosing K sufficiently large. Thus (5.14) and (5.18) imply that, for every $\epsilon > 0$, we can choose $K \in \mathbb{N}$ such that

$$\mathbb{1}(\mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}| = 0, |\hat{\mathcal{S}}| > K) < \epsilon) \xrightarrow[n \rightarrow \infty]{p_\nu} 1. \quad (5.19)$$

Finally, note that

$$\begin{aligned} \mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}| = 0, |\hat{\mathcal{S}}| > K) &= \mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}| = 0) - \mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}| = 0, |\hat{\mathcal{S}}| \leq K) \\ &= \mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}| = 0) - \mathbb{P}_\omega(|\hat{\mathcal{S}}| \leq K) \end{aligned}$$

for all sufficiently large n . Similarly, since $|\mathcal{S}| \geq |\hat{\mathcal{S}}|$,

$$\mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}| = 0, |\mathcal{S}| > K) = \mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}| = 0) - \mathbb{P}_\omega(|\mathcal{S}| \leq K)$$

for all sufficiently large n . Hence, by Lemma 5.9,

$$\mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}| = 0, |\hat{\mathcal{S}}| > K) - \mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}| = 0, |\mathcal{S}| > K) \xrightarrow[n \rightarrow \infty]{p_\nu} 0,$$

whence the lemma follows from (5.19). \square

For the remainder of the proof of Theorem 5.2, we re-analyze an exploration process of the forward epidemic process and we couple it to a multi-type branching process, such that the epidemic process is bigger than the branching process for as long as the total weight of both the vertices and the clique vertices in the exploration process is less than a predefined fraction of the total weight. The survival probability of this branching process can be made arbitrarily close to the probability of a large outbreak as $n \rightarrow \infty$. After that we ‘glue’ the susceptibility sets, if they are large, to the forward epidemic process.

We need some extra notation. Since the weights of the vertices are exchangeable, the model does not change if we order the vertices such that $A_i^{(n)} \leq A_{i+1}^{(n)}$, and $B_j^{(n)} \leq B_{j+1}^{(n)}$, for $1 \leq i < n$ and $1 \leq j < \lfloor \alpha n \rfloor$. For $\gamma \in (0, 1)$, we define

$$\begin{aligned} R^{(n)}(\gamma) &= \inf \left(i \leq n : \frac{\sum_{j=1}^i A_j}{L^{(n)}} \geq 1 - \gamma \right) \quad \text{and} \\ R'^{(n)}(\gamma) &= \inf \left(i \leq \lfloor \alpha n \rfloor : \frac{\sum_{j=1}^i B_j}{L'^{(n)}} \geq 1 - \gamma \right). \end{aligned}$$

Furthermore, define

$$\begin{aligned} \bar{\gamma} &= \bar{\gamma}(\gamma, n) = 1 - \frac{\sum_{j=1}^{R^{(n)}(\gamma)} A_j}{L^{(n)}} \quad \text{and} \\ \bar{\gamma}' &= \bar{\gamma}'(\gamma, n) = 1 - \frac{\sum_{j=1}^{R'^{(n)}(\gamma)} B_j}{L'^{(n)}}. \end{aligned}$$

We claim that, for $\gamma \in (0, 1)$, $\bar{\gamma} \xrightarrow[n \rightarrow \infty]{p_\nu} \gamma$. This can be seen by the following reasoning. Let $x = \inf(y \geq 0 : \mu^{-1} \mathbb{E}[A \mathbf{1}(A < y)] > 1 - \gamma/2)$. Then x is finite, since $\mu = \mathbb{E}[A] < \infty$. By the strong law of large numbers, we have $n^{-1} \sum_{i=1}^n A_i \mathbf{1}(A_i \leq x) \xrightarrow{a.s.} \mathbb{E}[A \mathbf{1}(A \leq x)]$ and $n^{-1} L^{(n)} \xrightarrow{a.s.} \mu$ as $n \rightarrow \infty$. Thus,

$$\frac{\sum_{i=1}^n A_i \mathbf{1}(A_i \leq x)}{L^{(n)}} \xrightarrow{a.s.} \mu^{-1} \mathbb{E}[A \mathbf{1}(A \leq x)] \geq 1 - \gamma/2$$

as $n \rightarrow \infty$, whence $\nu(A_{R^{(n)}} \leq x) \rightarrow 1$ as $n \rightarrow \infty$. Combining this with

$$1 - \bar{\gamma} = \frac{\sum_{j=1}^{R^{(n)}(\gamma)} A_j}{L^{(n)}} \geq 1 - \gamma$$

and

$$1 - \bar{\gamma} - \frac{A_{R^{(n)}}}{L^{(n)}} = \frac{\sum_{j=1}^{R^{(n)}(\gamma)-1} A_j}{L^{(n)}} < 1 - \gamma$$

completes the proof of the claim. Similarly we can prove that $\bar{\gamma}' \xrightarrow[n \rightarrow \infty]{p_\nu} \gamma$. This also shows that the vertices in $V^{(n)} \setminus \hat{V}^{(n)}$ (respectively, $V'^{(n)} \setminus \hat{V}'^{(n)}$) all have labels exceeding $R^{(n)}(\gamma)$ (respectively, $R'^{(n)}(\gamma)$) with probability tending to 1 as $n \rightarrow \infty$.

For $c_1 > 0$, let $I(c_1)$ be the set of vertices with type/infectious period less than c_1 . Let $\mathcal{I}(c_1)$ denote a random variable having distribution function given by $\mathbb{P}(\mathcal{I}(c_1) \leq x) = \mathbb{P}(\mathcal{I} \leq x | \mathcal{I} \geq c_1)$, for $x \geq c_1$. We use the multi-type branching process $\mathcal{Z}^f(A^{(n)}, B^{(n)}, \mathcal{I}(c_1), \gamma)$, which is obtained from $\mathcal{Z}^f(A^{(n)}, B^{(n)}, \mathcal{I}(c_1))$ by:

- (i) Killing upon birth all children with A -weight strictly larger than the weight of vertex $R^{(n)}(\gamma)$. Children with A -weight equal to the weight of vertex $R^{(n)}(\gamma)$ are killed independently with probability given by the fraction of those vertices in $V^{(n)}$ having weight equal to the weight of vertex $R^{(n)}(\gamma)$ that also have label strictly larger than $R^{(n)}(\gamma)$.
- (ii) Killing upon birth all litters corresponding to local epidemics in cliques with B -weight strictly larger than the weight of vertex $R'^{(n)}(\gamma)$. Cliques with B -weight equal to the weight of clique $R'^{(n)}(\gamma)$ are killed independently with probability given by the fraction of those vertices in $V'^{(n)}$ having B -weight equal to the weight of clique $R'^{(n)}(\gamma)$ that also have label strictly larger than $R'^{(n)}(\gamma)$.

If A_1, A_2, \dots, A_n are distinct, which happens ν -almost surely if the distribution of A has no atoms, then (i) reduces to killing upon birth all children with A -weight strictly larger than the weight of vertex $R^{(n)}(\gamma)$. If $B_1, B_2, \dots, B_{\lfloor \alpha n \rfloor}$ are distinct then (ii) simplifies similarly.

We observe that the corresponding survival probability function (cf. Section 4) $\tilde{\rho}(x; A^{(n)}, B^{(n)}, \mathcal{I}(c_1), \gamma)$ increases as $\gamma \downarrow 0$. Thus, the limit function, as $\gamma \downarrow 0$, exists and satisfies (4.3) by the monotone convergence theorem. Invoking Lemma 4.1, this limit function is

$$\lim_{\gamma \downarrow 0} \tilde{\rho}(x; A^{(n)}, B^{(n)}, \mathcal{I}(c_1), \gamma) = \tilde{\rho}(x; A^{(n)}, B^{(n)}, \mathcal{I}(c_1)).$$

Similarly, since $\tilde{\rho}(x; A^{(n)}, B^{(n)}, \mathcal{I}(c_1))$ is decreasing as $c_1 \downarrow 0$, one can show that

$$\lim_{c_1 \downarrow 0} \tilde{\rho}(x; A^{(n)}, B^{(n)}, \mathcal{I}(c_1)) = \tilde{\rho}(x; A^{(n)}, B^{(n)}, \mathcal{I}).$$

For $\rho(A^{(n)}, B^{(n)}, \mathcal{I})$ as in Section 4, this leads to the first assertion of the following lemma. The second assertion then follows using Lemma 5.5.

Lemma 5.11. *For every $\epsilon > 0$, $\omega \in \Omega$ and $n \in \mathbb{N}$, there exist $\gamma > 0$ and $c_1 > 0$ small enough such that*

$$|\rho(A^{(n)}, B^{(n)}, \mathcal{I}(c_1), \gamma) - \rho(A^{(n)}, B^{(n)}, \mathcal{I})| < \epsilon/2.$$

For every $\epsilon > 0$, there exist $\gamma > 0$ and $c_1 > 0$ such that

$$\mathbb{1}(|\rho(A^{(n)}, B^{(n)}, \mathcal{I}(c_1), \gamma) - \rho(A, B, \mathcal{I})| < \epsilon) \xrightarrow[n \rightarrow \infty]{p_\nu} 1.$$

Let $c_1 > 0$ and $\gamma \geq 0$ be constants. We consider the forward epidemic process $\bar{\mathcal{R}}^{(n, \gamma)} = \bar{\mathcal{R}}^{(n)}(\omega, \mathcal{I}, c_1, \gamma/3)$, which is obtained from $\mathcal{R}^{(n)}(\omega, \mathcal{I})$ by removing all vertices (and adjacent edges) in $I(c_1)$, $K^1(t_n)$ and $K^2(t_n)$ and not allowing for contacts in the cliques $K'^1(t_n)$ and $K'^2(t_n)$ or in cliques with label $R'^{(n)}(\gamma/3)$ or larger. As before, we deduce that for every $\gamma > 0$ and large enough n , all vertices in $V'^{(n)} \setminus \hat{V}^{(n)}$ have label at least $R'^{(n)}(\gamma/3)$, with probability arbitrarily close to 1. Also define $\bar{\mathcal{R}}^{(n)} = \bar{\mathcal{R}}^{(n, 0)} = \bar{\mathcal{R}}(\omega, \mathcal{I}, c_1, 0)$ and let the total weight of the cliques in $\bar{\mathcal{R}}^{(n)}$ (i.e. in the set of ultimately recovered vertices in $\bar{\mathcal{R}}^{(n)}$) be denoted by $\bar{\mathcal{W}}'^{(n)}(c_1)$.

Lemma 5.12. *For every $\epsilon > 0$, there exist constants $\eta > 0$ and $c_1 > 0$, such that*

$$\mathbb{1}(\mathbb{P}_\omega(\bar{\mathcal{W}}'^{(n)}(c_1) > \eta n) - (\rho(A, B, \mathcal{I}) - \epsilon) > 0) \xrightarrow[n \rightarrow \infty]{p_\nu} 1.$$

Proof. We explore $\bar{\mathcal{R}}^{(n, \gamma)}$ vertex by vertex (and clique by clique) and couple this with an exploration process of the tree of the branching process

$$\mathcal{Z}^{(n, \gamma)} = \mathcal{Z}^f(\hat{A}^{(n)}, \hat{B}^{(n)}, \mathcal{I}(c_1), \gamma).$$

With some abuse of notation we use $\bar{\mathcal{R}}^{(n, \gamma)}$ and $\mathcal{Z}^{(n, \gamma)}$ for the exploration processes as well.

We choose one vertex uniformly at random from $\hat{V}^{(n)}$. We assume that this vertex is not in $K^1(t_n)$ or $K^2(t_n)$ and that its type/infectious period exceeds c_1 . The probability that this assumption is met can be made arbitrarily close to 1 by choosing n large enough and c_1 small enough. Denote this vertex by \bar{v}_0 . Define the ‘forbidden sets’ of vertices by

$$\begin{aligned} \Gamma_0 &= K^1(t_n) \cup K^2(t_n) \cup I(c_1) \cup (V^{(n)} \setminus \hat{V}^{(n)}) \cup \{\bar{v}_0\} \quad \text{and} \\ \Gamma'_0 &= K'^1(t_n) \cup K'^2(t_n) \cup \{v'_i \in V'^{(n)} : i \geq R'^{(n)}(\gamma/3)\}. \end{aligned}$$

For the vertices in $V^{(n)} \setminus \Gamma_0$, we re-randomize the infectious period in such a way that, for every vertex in $V^{(n)} \setminus \Gamma_0$, we let it be an independent random variable with distribution $\mathcal{I}(c_1)$. This will not affect the distribution of the processes.

Let $\sigma_0^{(n)}(i)$ be a relabeling of the vertices in $V^{(n)}$ such that if $v_j \in \Gamma_0$ and $v_i \in V^{(n)} \setminus \Gamma_0$, then $\sigma_0^{(n)}(i) < \sigma_0^{(n)}(j)$, while if $v_i, v_j \in V^{(n)} \setminus \Gamma_0$, then $\sigma_0^{(n)}(i) < \sigma_0^{(n)}(j)$ if $i < j$. The precise order of the labels of the vertices in the forbidden set is not important. Define $\sigma_0'^{(n)}(i)$ similarly.

The A -weight and type of \bar{v}_0 are also assigned to the ancestor of $\mathcal{Z}^{(n, \gamma)}$, say that the A -weight is a_0 . Then we use a $\mathcal{P}(a_0 L'^{(n)} / (\mu n))$ random variable, d_0 , to denote the ‘maximal’

number of cliques vertex \bar{v}_0 is part of and, coupled to this, the ‘maximal’ number of child cliques the vertex has in $\mathcal{Z}^{(n,\gamma)}$. The meaning of maximal is clarified below.

We now identify the first child clique. Choose a real number, x' say, uniformly at random from the unit interval. In $\bar{\mathcal{R}}^{(n,\gamma)}$ we try to connect vertex \bar{v}_0 to the clique with label i , which satisfies

$$\sum_{j \in \mathbb{N}: \sigma_0'^{(n)}(j) < \sigma_0'^{(n)}(i)} B_j < x' L'^{(n)} \leq \sum_{j \in \mathbb{N}: \sigma_0'^{(n)}(j) \leq \sigma_0'^{(n)}(i)} B_j.$$

Let this vertex be \bar{v}_1' . The B -weight of the corresponding possible litter in $\mathcal{Z}^{(n,\gamma)}$ is B_i , where i is such that $\sum_{j=1}^{i-1} B_k < x' L'^{(n)} \leq \sum_{j=1}^i B_j$. If $\bar{v}_1' \in \Gamma'_0$, then the clique is ignored in $\bar{\mathcal{R}}^{(n,\gamma)}$. If $x > 1 - \bar{\gamma}$, then the litter in $\mathcal{Z}^{(n,\gamma)}$ is ignored. We note that as long as the weight of Γ'_0 is less than $\bar{\gamma} L'^{(n)}$, a clique can be ignored in $\bar{\mathcal{R}}^{(n,\gamma)}$ only if the corresponding litter in $\mathcal{Z}^{(n,\gamma)}$ is also ignored. Furthermore, the B -weight of the litter in $\mathcal{Z}^{(n,\gamma)}$ is not larger than the B -weight of the clique in $\bar{\mathcal{R}}^{(n,\gamma)}$.

Let the label of \bar{v}_1' be k . We now define

$$\sigma_1'^{(n)}(i) = \begin{cases} \sigma_0'^{(n)}(i), & \text{for } i \text{ such that } \sigma_0'^{(n)}(i) < \sigma_0'^{(n)}(k), \\ \sigma_0'^{(n)}(i) - 1, & \text{for } i \text{ such that } \sigma_0'^{(n)}(i) > \sigma_0'^{(n)}(k), \\ \lfloor \alpha n \rfloor, & \text{for } i = k. \end{cases}$$

That is, we give \bar{v}_1' the maximal label and keep the order of the labels of the other vertices. Furthermore, we add \bar{v}_1' to the forbidden set, i.e. set $\Gamma'_1 = \Gamma'_0 \cup \{\bar{v}_1'\}$. We choose the next clique in $\bar{\mathcal{R}}^{(n,\gamma)}$ and corresponding litter in $\mathcal{Z}^{(n,\gamma)}$, say \bar{v}_2' , in the same way as we choose \bar{v}_1' , with $\sigma_0'^{(n)}$ replaced by $\sigma_1'^{(n)}$ and Γ'_0 replaced by Γ'_1 , and we continue this process until we have identified all cliques that \bar{v}_0 is part of.

We then pick one of the cliques added to $\bar{\mathcal{R}}^{(n,\gamma)}$ whose corresponding litter was not ignored in $\mathcal{Z}^{(n,\gamma)}$. We realise a local epidemic in this group as follows. Assume that the B -weight of the clique is \bar{b}_1 . Then let d'_1 be $\mathcal{P}(\bar{b}_1 L^{(n)} / (\mu n))$. Consider a population with d'_1 initial susceptible individuals and 1 initial infectious individual, all with infectious period distributed as $\mathcal{I}(c_1)$, and couple two continuous time epidemics in this population as follows. Consider the first newly infected individual in this population. We associate this individual with vertices in $\bar{\mathcal{R}}^{(n,\gamma)}$ and in $\mathcal{Z}^{(n,\gamma)}$ as follows. Choose a real number, say x , uniformly at random from the unit interval. In $\bar{\mathcal{R}}^{(n,\gamma)}$, we try to connect clique \bar{v}_1' to the vertex with label i , which satisfies

$$\sum_{j \in \mathbb{N}: \sigma_0^{(n)}(j) < \sigma_0^{(n)}(i)} B_j < x L^{(n)} \leq \sum_{j \in \mathbb{N}: \sigma_0^{(n)}(j) \leq \sigma_0^{(n)}(i)} B_j.$$

Suppose that this vertex is \bar{v}_2 . The A -weight of the possible child in $\mathcal{Z}^{(n,\gamma)}$ is A_i , where i is such that $\sum_{j=1}^{i-1} A_j < x L^{(n)} \leq \sum_{j=1}^i A_j$. The vertex we choose is denoted by \bar{v}_1 .

If $\bar{v}_1 \in \Gamma_0$, then the vertex is ignored in $\bar{\mathcal{R}}^{(n,\gamma)}$ and immediately killed. If $x > 1 - \bar{\gamma}$, then the child in $\mathcal{Z}^{(n,\gamma)}$ is ignored. We note that as long as the weight of Γ_0 is less than $\bar{\gamma} L^{(n)}$, a vertex can be ignored in $\bar{\mathcal{R}}^{(n,\gamma)}$ only if the child in $\mathcal{Z}^{(n,\gamma)}$ is also ignored. Furthermore, the A -weight of the vertex in $\mathcal{Z}^{(n,\gamma)}$ is not larger than the A -weight of the vertex in $\bar{\mathcal{R}}^{(n,\gamma)}$. We identify the other vertices infected by local epidemics started by v_0 and the corresponding

children in $\mathcal{Z}^{(n,\gamma)}$ as we have identified the cliques v_0 is part of, where at each step the forbidden set of vertices might grow and the chosen vertex gets the highest label for the next vertex pick. The infectious period/type assigned to every vertex (which is not immediately killed) is distributed as $\mathcal{I}(c_1)$ and coupled vertices get the same infectious period/type. We continue in this way until we have identified all vertices infected by local epidemics started by v_0 and we then explore the cliques those individuals are part of one by one, as before.

The exploration process $\bar{\mathcal{R}}^{(n,\gamma)}$ dominates the exploration process $\mathcal{Z}^{(n,\gamma)}$ until the total weight of the forbidden set in $V^{(n)}$ in $\bar{\mathcal{R}}^{(n,\gamma)}$ is at least $\bar{\gamma}L^{(n)}$ or the total weight of the forbidden set in $V'^{(n)}$ in $\bar{\mathcal{R}}^{(n,\gamma)}$ is at least $\bar{\gamma}L'^{(n)}$.

Note that we may choose $c_1 > 0$ small enough such that $\mathbb{P}(\mathcal{I} < c_1) < \gamma/2$. By the law of large numbers this implies that $c_1 > 0$ might be chosen such that the total weight of vertices in $I(c_1)$ is less than $(\gamma/2)L^{(n)}$ with probability tending to 1 as $n \rightarrow \infty$. By Lemma 5.7, we know that the weights of K^1, K^2, K'^1 and K'^2 are each a.s. $o(n)$ and we know that the set of vertices with label $\geq R'^{(n)}(\gamma/3)$ has total weight at least $(\gamma/3)L^{(n)}$ and the probability that this total weight is less than $(\gamma/2)L^{(n)}$ can be made arbitrary close to 1 by choosing n sufficiently large.

If the ordering of the exploration processes $\bar{\mathcal{R}}^{(n,\gamma)}$ and $\mathcal{Z}^{(n,\gamma)}$ stops because the total weight of the forbidden set in $V'^{(n)}$ exceeds $\gamma L'^{(n)}$, then, using Lemma 5.11, the lemma is immediate with $\eta = \gamma/3$. If this ordering stops because the total weight of the forbidden set in $V^{(n)}$ exceeds $\gamma L^{(n)}$, then the total weight of vertices in $\bar{\mathcal{R}}^{(n,\gamma)}$ that are not in the original forbidden set exceeds $(\gamma/3)L^{(n)}$. We now proceed as follows. Since all of the vertices in $\hat{V}'^{(n)}$ have weight at most $\log n$, the number of vertices with labels exceeding $R'^{(n)}(\gamma/3)$ grows to infinity and, by the law of large numbers, we find that the total weight of cliques in this set which contain vertices in $\bar{\mathcal{R}}^{(n,\gamma)}$ is $\Theta(n)$. This completes the proof of the lemma. \square

Proof of Theorem 5.2. We use the notation of Lemma 5.12. Recall that $\bar{\mathcal{R}}^{(n)} = \bar{\mathcal{R}}^{(n,0)}$ and that $\mathcal{R}^{(n)} = \mathcal{R}^{(n)}(\omega, \mathcal{I})$ is the set of ultimately infected vertices in a population of n individuals.

We first provide bounds for

$$\begin{aligned} \mathbb{E}_\omega[n^{-1}|\mathcal{R}^{(n)}| \mid \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n] &= \mathbb{E}_\omega[n^{-1} \sum_{i=1}^n \mathbf{1}(v_i \in \mathcal{R}^{(n)}) \mid \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n] \\ &= \mathbb{P}_\omega(v_1 \in \mathcal{R}^{(n)} \mid \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n) \end{aligned}$$

and for

$$\begin{aligned} \mathbb{E}_\omega[n^{-2}|\mathcal{R}^{(n)}|^2 \mid \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n] &= \mathbb{E}_\omega[n^{-2} \sum_{i=1}^n \sum_{j=1}^n \mathbf{1}(v_i, v_j \in \mathcal{R}^{(n)}) \mid \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n] \\ &= n^{-1} \mathbb{P}_\omega(v_1 \in \mathcal{R}^{(n)} \mid \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n) \\ &\quad + (1 - n^{-1}) \mathbb{P}_\omega(v_1, v_2 \in \mathcal{R}^{(n)} \mid \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n). \end{aligned}$$

Let $\epsilon' > 0$. By Lemma 5.8 and the asymptotic theory of supercritical general branching processes [24] modified to the lattice case, we have that, if the susceptibility set of v_1 in $\hat{G}^{(n)}$ survives for $t_n = \lceil \log \log n \rceil$ generations, then there exists $c_2 > 0$ such that the

probability that the number and the total weight of the vertices in this generation is at least $c_2 \log \log n$ is greater than $1 - \epsilon'$ for all sufficiently large n . We denote the set of vertices in generation t_n of this susceptibility set by $\hat{V}_{t_n}^{(n)}$. The same holds for the susceptibility set of v_2 . Furthermore, the events of survival up to generation t_n of the two susceptibility sets are asymptotically independent by a birthday problem type of argument and Lemma 5.7.

Conditioned on $\bar{\mathcal{W}}'^{(n)}(c_1) > \eta n$, the law of large numbers establishes that the following event occurs with probability exceeding $1 - \epsilon'$. The number of vertices in $\hat{V}_{t_n}^{(n)}$ that both (i) are in the same clique as an infected vertex explored in $\bar{\mathcal{R}}^{(n)}$ and (ii) have infectious period at least c_1 , grows to infinity as $n \rightarrow \infty$. Since each vertex in $\hat{V}_{t_n}^{(n)}$ is infected independently with probability at least $1 - e^{-c_1} > 0$, we have that

$$\mathbb{1} \left(\mathbb{P}_\omega \left(v_1 \in \mathcal{R}^{(n)} \mid |\hat{\mathcal{S}}_{t_n}^1| > 0, \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n \right) > 1 - 2\epsilon' \right) \xrightarrow[n \rightarrow \infty]{p_\nu} 1.$$

Furthermore, if the susceptibility set of v_1 does not survive up to generation t_n in $\hat{G}^{(n)}$, then Lemma 5.10 shows that the probability that the initial infective is in v_1 's susceptibility set converges to 0. More precisely, for every $K \in \mathbb{N}$ we have that

$$\begin{aligned} \mathbb{P}_\omega(v_1 \in \mathcal{R}^{(n)} \mid |\hat{\mathcal{S}}_{t_n}^1| = 0) &= \frac{\mathbb{P}_\omega(v_1 \in \mathcal{R}^{(n)}, |\hat{\mathcal{S}}_{t_n}^1| = 0)}{\mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}^1| = 0)} \\ &\leq \frac{\mathbb{P}_\omega(v_1 \in \mathcal{R}^{(n)}, |\mathcal{S}^1| \leq K) + \mathbb{P}_\omega(|\mathcal{S}^1| > K, |\hat{\mathcal{S}}_{t_n}^1| = 0)}{\mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}^1| = 0)}. \end{aligned}$$

The first term in the numerator of the right hand side of this inequality converges to 0 as $n \rightarrow \infty$, while by Lemma 5.10 we have that, for every $\epsilon > 0$ and $\delta > 0$, there exists $K \in \mathbb{N}$ such that the second term in the numerator is smaller than ϵ with ν -probability at least $1 - \delta$ for all sufficiently large n . The denominator is trivially strictly positive. We therefore conclude that

$$\mathbb{P}_\omega(v_1 \in \mathcal{R}^{(n)} \mid |\hat{\mathcal{S}}_{t_n}^1| = 0) \xrightarrow[n \rightarrow \infty]{p_\nu} 0.$$

From the proof of Lemma 5.12 we deduce that

$$\mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}^1| > 0) - \mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}^1| > 0 \mid \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n) \xrightarrow[n \rightarrow \infty]{p_\nu} 0,$$

whence

$$\mathbb{P}_\omega(v_1 \in \mathcal{R}^{(n)} \mid \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n) - \mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}^1| > 0) \xrightarrow[n \rightarrow \infty]{p_\nu} 0.$$

Now, arguing as at the start of the proof of Lemma 5.8,

$$\mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}^1| > 0) - \mathbb{P}_\omega(|\mathcal{Z}_{t_n}^b(A^{(n)}, B^{(n)}, \mathcal{I})| > 0) \xrightarrow[n \rightarrow \infty]{p_\nu} 0,$$

whilst the end of the proof of Lemma 5.8 shows that

$$\mathbb{P}_\omega(|\mathcal{Z}_{t_n}^b(A^{(n)}, B^{(n)}, \mathcal{I})| > 0) \xrightarrow[n \rightarrow \infty]{p_\nu} \rho^b(A, B, \mathcal{I}).$$

Thus, $\mathbb{P}_\omega(|\hat{\mathcal{S}}_{t_n}^1| > 0) \xrightarrow[n \rightarrow \infty]{p_\nu} \rho^b(A, B, \mathcal{I})$, whence

$$\mathbb{E}_\omega[n^{-1}|\mathcal{R}^{(n)}| \mid \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n] \xrightarrow[n \rightarrow \infty]{p_\nu} \rho^b(A, B, \mathcal{I}).$$

Since the first t_n generations of the susceptibility sets of v_1 and v_2 in $\hat{G}^{(n)}$ are non-overlapping with probability tending to 1 as $n \rightarrow \infty$, we notice that

$$\mathbb{P}_\omega(v_1, v_2 \in \mathcal{R}^{(n)} \mid \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n) - (\mathbb{P}_\omega(v_1 \in \mathcal{R}^{(n)} \mid \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n))^2 \xrightarrow[n \rightarrow \infty]{p_\nu} 0.$$

This gives that

$$\mathbb{E}_\omega[n^{-2}|\mathcal{R}^{(n)}|^2 \mid \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n] \xrightarrow[n \rightarrow \infty]{p_\nu} (\rho^b(A, B, \mathcal{I}))^2.$$

Therefore, $\text{var}(n^{-1}|\mathcal{R}^{(n)}| \mid \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n) \xrightarrow[n \rightarrow \infty]{p_\nu} 0$ and we conclude that, for all $\delta > 0$,

$$\mathbb{P}_\omega(|n^{-1}|\mathcal{R}^{(n)}| - \rho^b(A, B, \mathcal{I})| < \delta \mid \bar{\mathcal{W}}'^{(n)}(c_1) > \eta n) \xrightarrow[n \rightarrow \infty]{p_\nu} 1. \quad (5.20)$$

On the other hand, we know by Lemma 5.12 that for every $\epsilon' > 0$, there exist constants $\eta > 0$ and $c_1 > 0$ such that

$$\mathbb{1}(\mathbb{P}_\omega(\bar{\mathcal{W}}'^{(n)}(c_1) > \eta n) > \rho(A, B, \mathcal{I}) - \epsilon') \xrightarrow[n \rightarrow \infty]{p_\nu} 1. \quad (5.21)$$

Furthermore, by Theorem 5.1 there exists $k \in \mathbb{N}$ such that

$$\mathbb{1}\left(\sum_{i=1}^k \mathbb{P}_\omega(|\mathcal{R}^{(n)}| = i) > 1 - \rho(A, B, \mathcal{I}) - \epsilon'\right) \xrightarrow[n \rightarrow \infty]{p_\nu} 1. \quad (5.22)$$

Now observe that

$$\begin{aligned} \mathbb{P}_\omega(v_1 \in \mathcal{R}^{(n)}, \bar{\mathcal{W}}'^{(n)}(c_1) \leq \eta n) &\leq \mathbb{P}_\omega(v_1 \in \mathcal{R}^{(n)}, |\mathcal{R}^{(n)}| \leq k) \\ &\quad + \mathbb{P}_\omega(\bar{\mathcal{W}}'^{(n)}(c_1) \leq \eta n, |\mathcal{R}^{(n)}| > k). \end{aligned}$$

By exchangeability, the first term on the right hand side of this inequality is bounded above by k/n which converges to 0 as $n \rightarrow \infty$. Further, for any $K \in \mathbb{N}$,

$$\mathbb{P}_\omega(\bar{\mathcal{W}}'^{(n)}(c_1) > \eta n, |\mathcal{R}^{(n)}| \leq K) \xrightarrow[n \rightarrow \infty]{p_\nu} 0,$$

so (5.21) and (5.22) imply that for every $\epsilon > 0$, there exists $k \in \mathbb{N}$ such that

$$\mathbb{1}(\mathbb{P}_\omega(\bar{\mathcal{W}}'^{(n)}(c_1) \leq \eta n, |\mathcal{R}^{(n)}| > k) < \epsilon) \xrightarrow[n \rightarrow \infty]{p_\nu} 1.$$

It follows that

$$\mathbb{E}_\omega[n^{-1}|\mathcal{R}^{(n)}| \mid \bar{\mathcal{W}}'^{(n)}(c_1) \leq \eta n] \xrightarrow[n \rightarrow \infty]{p_\nu} 0,$$

so for every $\delta > 0$ we have

$$\mathbb{P}_\omega(n^{-1}|\mathcal{R}^{(n)}| < \delta \mid \bar{\mathcal{W}}'^{(n)}(c_1) \leq \eta n) \xrightarrow[n \rightarrow \infty]{p_\nu} 1. \quad (5.23)$$

Combining (5.20) and (5.23) completes the proof of Theorem 5.2. \square

6 Extension

In this paper we study the spread of an SIR epidemic on a random intersection graph. A variant of the random intersection graph is proposed in [26], where a configuration model construction is used to create the graph. In our terminology and notation, independent degrees are assigned to vertices in V and V' , where the degrees of vertices in V are each distributed as a random variable D and the degrees of vertices in V' are each distributed as a random variable H . Each vertex in $V \cup V'$ is assigned a number of half-edges given by its degree. In the auxiliary graph $\mathbb{A}^{(n)}$ the half-edges of the first n vertices in V are paired uniformly at random with the first $L^{(n)}$ half-edges in V' , where $L^{(n)}$ is the number of half-edges assigned to the first n vertices in V . Note that the final vertex in V' used in this construction might not retain its full degree in $\mathbb{A}^{(n)}$.

The forward and backward branching processes can be modified in the obvious fashion to this setting and equivalent formulae to the key expressions (B.6), (B.7) and (B.8) in Appendix B.2 can be derived, thus facilitating calculation of the threshold parameter R_* and survival probabilities of these branching processes. We expect that, under mild conditions on the distributions of D and H , theorems corresponding to Theorems 3.3–3.5 hold for this model. Some additional dependencies arise since connecting to a vertex takes away one of its available half-edges, however we anticipate that the impact of those dependencies is very small.

A Proof of Lemma 4.1

In order to prove Lemma 4.1 we use an idea from Riordan [33]. He considers the corresponding problem for a class of multitype branching processes having type space $(0, 1]$ in which, in crude terms, the number of children having type in any specified interval an individual of type x has tends to infinity as $x \downarrow 0$. We cannot use the result in [33] directly because the number of children an individual of type x has tends to zero as $x \downarrow 0$. However, we can apply the idea in [33] to a branching process that is intimately related to $\tilde{\mathcal{Z}}^f$, which we now describe, and exploit a connection between the functional $\Phi(\tilde{\rho})(x)$ and an equivalent functional for the new branching process to obtain the desired result.

Recall that in the branching process $\tilde{\mathcal{Z}}^f$, individuals arise in litters, with a litter being distributed as the set of individuals that are infected in a local (single-clique) epidemic, not including the individual who triggers that local epidemic. Consider such a local epidemic and suppose that the clique contains the initial infective, i^* say, and m susceptible individuals. The final outcome of the local epidemic can be obtained using the corresponding Epidemic Generated Graph, by first determining the number of individuals, a say, that are contacted directly by the initial infective, and then considering the epidemic, $\mathcal{E}_{s,a}$ say, triggered by those a individuals among the remaining $s = m - a$ susceptibles in the clique. Suppose that the epidemic $\mathcal{E}_{s,a}$ infects $T_{s,a}$ individuals, in addition to its a initial infectives. (Thus, in the notation of Section 3.2, $T(m) = a + T_{s,a}$.) Note that the infectious periods of the a initial infectives in $\mathcal{E}_{s,a}$ are i.i.d. copies of \mathcal{I} and also that, conditional upon the value of (s, a) , such epidemics in different cliques are mutually independent, even if they arise from the same initial infective i^* . Thus the epidemic $\mathcal{E}^{(n)}$ may be approximated by a branching process of litters, in which each litter is typed by its value of (s, a) and its

offspring are the litters triggered by the $a + T_{s,a}$ infectives in the corresponding $\mathcal{E}_{s,a}$. Let $\hat{\mathcal{Z}}^f$ be the branching process derived in this fashion corresponding to the branching process \mathcal{Z}^f . Clearly, litters with $a = 0$ are superfluous, so the type space for $\hat{\mathcal{Z}}^f$ may be taken to be $\hat{\mathcal{T}} = \{(s, a) : s \in \mathbb{Z}_+, a \in \mathbb{N}\}$.

We now derive the next-generation functional (i.e. the analogue of $\tilde{\Phi}(h)(x)$) associated with $\hat{\mathcal{Z}}^f$. For notational convenience we assume that \mathcal{I} has an absolutely continuous distribution, though this is not essential and the argument (and the proof of Lemma 4.1 below) can be extended to the general case. Let $\hat{h}(s, a) : \hat{\mathcal{T}} \rightarrow [0, 1]$ be a measurable test function and suppose that litters are marked independently with a dagger (to distinguish from the marks used on \mathcal{Z}^f), with a litter of type (s, a) being marked with probability $\hat{h}(s, a)$. Let $\hat{\Phi}(\hat{h})(s, a)$ be the probability that a litter of type (s, a) directly spawns at least one litter that is marked with a dagger.

Consider the epidemic $\mathcal{E}_{s,a}$ described above and suppose that $T_{s,a} = k$. Let $x_{-a+1}, x_{-a+2}, \dots, x_0$ and x_1, x_2, \dots, x_k denote the lengths of the infectious periods of the a initial infectives and the k subsequently infected individuals, respectively. Let $p_{s,a}(k; x_{-a+1}, x_{-a+2}, \dots, x_0, x_1, \dots, x_k)$ be the probability density that $T_{s,a} = k$ and the infectious periods are given by x_{-a+1}, \dots, x_k . Then,

$$\hat{\Phi}(\hat{h})(s, a) = 1 - \sum_{k=0}^s \int_{(0, \infty]^{a+k}} p_{s,a}(k; x_{-a+1}, \dots, x_k) \prod_{i=-a+1}^k P_{\hat{h}}(x_i) dx_{-a+1} \dots dx_k, \quad (\text{A.1})$$

where $P_{\hat{h}}(x)$ is the probability that an individual, i^* say, having infectious period of length x , does not spawn a litter which is marked with a dagger.

To determine $P_{\hat{h}}(x)$, note first that i^* belongs to $\tilde{X} \sim \mathcal{MP}(\tilde{A})$ cliques, not counting the clique it was infected through, and consider one such clique. Besides i^* , this clique contains $\tilde{Y} \sim \mathcal{MP}(\tilde{B})$ individuals. Suppose that $\tilde{B} = b$, then $\tilde{Y} \sim \mathcal{P}(b)$ and these \tilde{Y} individuals are infected independently by i^* , each with probability $1 - e^{-x}$. Thus, given $\tilde{B} = b$, the litter has type (s, a) , where s and a are independent realisations of the Poisson random variables $\mathcal{P}(be^x)$ and $\mathcal{P}(b(1 - e^{-x}))$, respectively. Hence, the unconditional probability that this litter is not marked with a dagger is

$$\mathbb{E} \left[\sum_{s=0}^{\infty} \sum_{a=0}^{\infty} \frac{(e^{-x} \tilde{B})^s}{s!} \frac{((1 - e^{-x}) \tilde{B})^a}{a!} e^{-\tilde{B}} (1 - \hat{h}(s, a)) \right],$$

where $\hat{h}(s, 0) = 0$ ($s \in \mathbb{Z}_+$). Given that i^* has infectious period x , the local epidemics it initiates in the above \tilde{X} cliques are independent, so

$$P_{\hat{h}}(x) = \phi_{\tilde{A}} \left(\mathbb{E} \left[\sum_{s=0}^{\infty} \sum_{a=0}^{\infty} \frac{(e^{-x} \tilde{B})^s}{s!} \frac{((1 - e^{-x}) \tilde{B})^a}{a!} e^{-\tilde{B}} \hat{h}(s, a) \right] \right). \quad (\text{A.2})$$

Let $\hat{\rho}(s, a)$ be the survival probability of the branching process $\hat{\mathcal{Z}}^f$, given that the initial litter has type (s, a) . Then $\hat{\rho}$ is the maximal solution of $\hat{\rho}(s, a) = \hat{\Phi}(\hat{\rho})(s, a)$. If either $s \rightarrow \infty$ or $a \rightarrow \infty$, then for any $(s', a') \in \hat{\mathcal{T}}$ and any $K \in \mathbb{N}$, the probability that a type- (s, a) individual has at least K type- (s', a') children in the next generation tends to 1. Furthermore, it is easy to deduce that for any $(s, a), (s', a') \in \hat{\mathcal{T}}$, the number of type- (s', a')

children an individual of type (s, a) begets is non-zero with positive probability, so $\hat{\mathcal{Z}}^f$ is irreducible. Using the same argument as in [33, pp. 911-912], we conclude that there is at most one non-zero solution of $\hat{\rho}(s, a) = \hat{\Phi}(\hat{\rho})(s, a)$.

Recall that Lemma 4.1 states that there is at most one non-zero solution $\tilde{\rho}(x)$ of the functional equation $\tilde{\rho}(x) = \tilde{\Phi}(\tilde{\rho})(x)$. To prove this it is useful to derive an alternative expression for $\tilde{\Phi}(h)(x)$. Suppose that the initial ancestor, i^* say, in $\tilde{\mathcal{Z}}^f$ has infectious period of length x . By conditioning on the size of and the number of people directly infected by i^* in a given clique, the probability that i^* has no marked child in that clique is given by

$$\mathbb{E} \left[\sum_{s=0}^{\infty} \sum_{a=0}^{\infty} \frac{(e^{-x}\tilde{B})^s}{s!} \frac{((1-e^{-x})\tilde{B})^a}{a!} e^{-\tilde{B}} A(s, a, h) \right], \quad (\text{A.3})$$

where

$$A(s, a, h) = \sum_{k=0}^s \int_{(0, \infty]^{a+k}} p_{s,a}(k; x_{-a+1}, \dots, x_k) \prod_{i=-a+1}^k (1 - h(x_i)) dx_{-a+1} \cdots dx_k, \quad (\text{A.4})$$

whence, since i^* belongs to $\tilde{X} \sim \mathcal{MP}(\tilde{A})$ further cliques (in addition to the one it was infected through),

$$\tilde{\Phi}(h)(x) = 1 - \phi_{\tilde{A}} \left(\mathbb{E} \left[\sum_{s=0}^{\infty} \sum_{a=0}^{\infty} \frac{(e^{-x}\tilde{B})^s}{s!} \frac{((1-e^{-x})\tilde{B})^a}{a!} e^{-\tilde{B}} (1 - A(s, a, h)) \right] \right). \quad (\text{A.5})$$

Suppose that

$$h(x) = \tilde{\Phi}(h)(x). \quad (\text{A.6})$$

Then (A.5) and (A.4) imply that

$$A(s, a, h) = \sum_{k=0}^s \int_{(0, \infty]^{a+k}} p_{s,a}(k; x_{-a+1}, \dots, x_k) \times \prod_{i=-a+1}^k \phi_{\tilde{A}} \left(\mathbb{E} \left[\sum_{s_i=0}^{\infty} \sum_{a_i=0}^{\infty} \frac{(e^{-x_i}\tilde{B})^{s_i}}{s_i!} \frac{((1-e^{-x_i})\tilde{B})^{a_i}}{a_i!} e^{-\tilde{B}} (1 - A(s_i, a_i, h)) \right] \right) dx_{-a+1} \cdots dx_k.$$

Thus, by (A.1) and (A.2), if h is treated as fixed, $\hat{h}(s, a) = 1 - A(s, a, h)$ satisfies

$$\hat{h}(s, a) = \hat{\Phi}(\hat{h})(s, a). \quad (\text{A.7})$$

Let h be a non-zero (i.e. not identically zero) solution of (A.6), assuming such a solution exists. Then \hat{h} must be the unique non-zero solution of (A.7), $\hat{\rho}$ say. (Note that if \hat{h} is identically zero then (A.5) and (A.6) imply that h is identically zero.) Thus $\hat{h}(s, a) = 1 - A(s, a, h)$ is independent of h , and $h(x)$ is given by the right hand side of (A.5) with $A(s, a, h)$ replaced by $1 - \hat{\rho}(s, a)$, which proves the lemma.

B Calculation of properties of forward and backward branching processes

In this appendix we give expressions for properties of the forward and backward branching processes, \mathcal{Z}^f and \mathcal{Z}^b , which enable the threshold parameter R_* and the survival probabilities ρ and ρ^b which appear in Theorem 3.5 to be computed. These expressions rest on results for the final outcome of homogeneously mixing SIR epidemic models. In a series of papers, see for example [31], Lefèvre and Picard showed that many quantities related to the final outcome of an SIR epidemic can be expressed compactly in terms of Gontcharoff polynomials, and these were extended by Ball and O'Neill [6] to include so-called general final state random variables. The latter are required to compute functionals associated with the forward branching process \mathcal{Z}^f . Results for homogeneously mixing SIR epidemic models are outlined in Section B.1 and their application to computing properties of \mathcal{Z}^f and \mathcal{Z}^b is described in Section B.2.

B.1 Results for homogeneously mixing populations

In this section we give a restatement of Theorem 4.2 from Ball and O'Neill [6], adapted to the purposes of this paper (cf. [8]). We note that Ball and O'Neill provide appreciably more general results than their Theorem 4.2. In order to state the theorem, we need the following notation. We consider an SIR epidemic in a homogeneously mixing population with s initial susceptible individuals and a initial infectious individuals. The initial susceptible individuals are labeled $1, 2, \dots, s$ and the initial infectious individuals have labels $-a + 1, -a + 2, \dots, 0$. The random variable \mathcal{I}_i represents the infectious period that individual i will have if it becomes infected. Thus, the probability that individual i , if infected, ultimately has an infectious contact with individual j is $1 - e^{-\mathcal{I}_i}$. (As before, infectious contacts between pairs of individuals are governed by independent unit-rate Poisson processes.) We assume that the random variables $(\mathcal{I}_i, i = -a + 1, -a + 2, \dots, s)$ are independent and all distributed as \mathcal{I} ; they are also independent of the Poisson processes describing infectious contacts. Note that this model is the epidemic $\mathcal{E}_{s,a}$ introduced in Appendix A. Let $\hat{h}(x) : (0, \infty] \rightarrow [0, \infty]$ be a measurable function (the relevant measures are clear from the context) and $\theta > 0$. Furthermore, let

$$\hat{U} = \hat{U}(\hat{h}, \theta) = (\hat{u}_i(\hat{h}, \theta), i \in \mathbb{Z}_+) = (\hat{u}_i, i \in \mathbb{Z}_+)$$

be an infinite vector, where $\hat{u}_k = \mathbb{E}[e^{-k\mathcal{I}}e^{-\theta\hat{h}(\mathcal{I})}]$. Let \mathcal{R} be the set of ultimately recovered individuals in $\mathcal{E}_{m,a}$, including the initial infectives as well as any initial susceptibles that become infected.

The Gontcharoff polynomials $G_m(x|\hat{U})$, $m \in \mathbb{Z}_+$, are defined recursively by

$$\frac{x^m}{m!} = \sum_{k=0}^m \frac{(\hat{u}_k)^{m-k}}{(m-k)!} G_k(x|\hat{U}), \quad (\text{B.1})$$

for $m \in \mathbb{Z}_+$. We note that $G_m(x|\hat{U})$ is a polynomial of order m , which depends on $\hat{u}_0, \hat{u}_1, \dots, \hat{u}_{m-1}$. Some properties of Gontcharoff polynomials are mentioned in Section 2

of [6]. In this paper we use only (B.1) and

$$G_m(x|\hat{U}) = \int_{\hat{u}_0}^x \int_{\hat{u}_1}^{\xi_0} \cdots \int_{\hat{u}_{m-1}}^{\xi_{m-2}} d\xi_{m-1} \cdots d\xi_1 d\xi_0, \quad (\text{B.2})$$

for $m \in \mathbb{Z}_+$. The following theorem is a special case of Theorem 4.2 in [6], which allows \hat{h} to be random.

Theorem B.1. *For \mathcal{R} , \hat{h} and \hat{U} as above, we have*

$$\mathbb{E}[x^{s+a-|\mathcal{R}|} e^{-\theta \sum_{i \in \mathcal{R}} \hat{h}(\mathcal{I}_i)}] = \sum_{k=0}^s \frac{s!}{(s-k)!} (\hat{u}_k)^{s-k+a} G_k(x|\hat{U}).$$

We use the following corollary of this theorem.

Corollary B.2. *Let $U = U(h) = (u_i(h), i \in \mathbb{Z}_+) = (u_i, i \in \mathbb{Z}_+)$, where $u_i = \mathbb{E}[e^{-i\mathcal{I}}(1 - h(\mathcal{I}))]$ and $h(x) : (0, \infty] \rightarrow [0, 1]$ is Borel-measurable, and let \mathcal{R} be as above. Then*

$$\mathbb{E}[\prod_{i \in \mathcal{R}} (1 - h(\mathcal{I}_i))] = \sum_{k=0}^s \frac{s!}{(s-k)!} (u_k)^{s-k+a} G_k(1|U). \quad (\text{B.3})$$

Proof. Set $x = \theta = 1$ and $\hat{h} = -\log(1 - h)$ in Theorem B.1. □

Recall the random variable $T(m)$ introduced in Section 3.2. In the present notation, $T(m)$ is the size of the epidemic $\mathcal{E}_{m,1}$, not including the initial infective. The mean of $T(m)$ can be expressed in terms of Gontcharoff polynomials as follows (see e.g. [4, equation (3.6)]):

$$\mathbb{E}[T(m)] = m - \sum_{k=1}^m \frac{m!}{(m-k)!} (v_{k-1})^{m+1-k} G_{k-1}(1|V) \quad (m = 1, 2, \dots), \quad (\text{B.4})$$

where $v_k = \mathbb{E}[e^{-(k+1)\mathcal{I}}]$ and $V = (v_i, i \in \mathbb{Z}_+)$.

The distribution of the size of the local susceptibility set of an individual can also be expressed using Gontcharoff polynomials. Recall from Section 3.3 that $S(m)$ is the size of the local susceptibility set of an individual in a clique of size $m+1$, where $S(m)$ does *not* include the individual in question. As in [8, Section 3], we have

$$\mathbb{P}(S(m) = k) = \frac{m!}{(m-k)!} (v_k)^{m-k} G_k(1|V) \quad (k = 0, 1, \dots, m), \quad (\text{B.5})$$

where v_k and V are as in (B.4).

B.2 Application to branching processes \mathcal{Z}^f and \mathcal{Z}^b

Let h be as in Corollary B.2 and suppose that individuals in $\mathcal{E}_{s,a}$ are marked independently, with individual i being marked with probability $h(\mathcal{I}_i)$ ($i = -a+1, -a+2, \dots, s$). Then (B.3) gives the probability that the epidemic $\mathcal{E}_{s,a}$ contains no marked infective. Recall from Section 4 that $F(h)(x)$ is the probability that the initial ancestor in \mathcal{Z}^f has at

least one marked child arising from the local epidemic in a given clique. Arguing as in the derivation of (A.3) gives, after repeatedly using Fubini's theorem (note that $G_k(1|U) > 0$ for all k , using (B.2) and the fact that $(u_k \in [0, 1])$ is decreasing in k),

$$\begin{aligned}
1 - F(h)(x) &= \mathbb{E} \left[\sum_{s=0}^{\infty} \sum_{a=0}^{\infty} \frac{e^{-xs} \tilde{B}^s}{s!} \frac{(1 - e^{-x})^a \tilde{B}^a}{a!} e^{-\tilde{B}} \sum_{k=0}^s \frac{s!}{(s-k)!} (u_k)^{s-k+a} G_k(1|U) \right] \\
&= \mathbb{E} \left[\sum_{s=0}^{\infty} \sum_{k=0}^s \frac{e^{-xs} \tilde{B}^s}{s!} \frac{s!}{(s-k)!} (u_k)^{s-k} G_k(1|U) e^{-\tilde{B}(1-u_k(1-e^{-x}))} \right] \\
&= \mathbb{E} \left[\sum_{k=0}^{\infty} \sum_{s=k}^{\infty} \frac{e^{-xs} \tilde{B}^s}{(s-k)!} (u_k)^{s-k} G_k(1|U) e^{-\tilde{B}(1-u_k(1-e^{-x}))} \right] \\
&= \mathbb{E} \left[\sum_{k=0}^{\infty} e^{-xk} \tilde{B}^k e^{-Y(1-u_k)} G_k(1|U) \right] \\
&= \sum_{k=0}^{\infty} (-e^{-x})^k \phi_{\tilde{B}}^{(k)} (1 - u_k) G_k(1|U),
\end{aligned} \tag{B.6}$$

where $\phi_{\tilde{B}}^{(k)}$ is the k th derivative of $\phi_{\tilde{B}}$.

Finally, we derive expressions for $\mathbb{E}_{\tilde{Y}}[\mathbb{E}[T(\tilde{Y})|\tilde{Y}]]$ and $\mathbb{E}_{\tilde{Y}}[f_{S(\tilde{Y})|\tilde{Y}}(s)]$, where $\tilde{Y} \sim \mathcal{MP}(\tilde{B})$, which are required to compute R_* and ρ^b , see (3.1) and (3.5), respectively. Recall that $(\tilde{Y}|\tilde{B} = b) \sim \mathcal{P}(b)$ and $\mathbb{E}[\tilde{Y}] = \mathbb{E}[\tilde{B}]$. Thus conditioning on \tilde{B} and using (B.4) yields

$$\mathbb{E}_{\tilde{Y}}[\mathbb{E}[T(\tilde{Y})|\tilde{Y}]] = \mathbb{E}[\tilde{B}] - \mathbb{E} \left[\sum_{m=1}^{\infty} \frac{\tilde{B}^m}{m!} e^{-\tilde{B}} \sum_{k=1}^m \frac{m!}{(m-k)!} (v_{k-1})^{m+1-k} G_{k-1}(1|V) \right].$$

Interchanging the order of summation then yields, after elementary algebra, that

$$\mathbb{E}_{\tilde{Y}}[\mathbb{E}[T(\tilde{Y})|\tilde{Y}]] = \mathbb{E}[\tilde{B}] - \sum_{k=1}^{\infty} v_{k-1} (-1)^k \phi_{\tilde{B}}^{(k)} (1 - v_{k-1}) G_k(1|V). \tag{B.7}$$

Turning to the size of the local susceptibility set of an individual in a typical clique, first note that conditioning on \tilde{B} and using (B.5) gives, for $k \in \mathbb{Z}_+$,

$$\begin{aligned}
\mathbb{P}(S(\tilde{Y}) = k) &= \mathbb{E} \left[\sum_{m=k}^{\infty} \frac{\tilde{B}^m}{m!} e^{-\tilde{B}} \frac{m!}{(m-k)!} (v_k)^{m-k} G_k(1|V) \right] \\
&= \mathbb{E} \left[\tilde{B}^k e^{-\tilde{B}(1-v_k)} G_k(1|V) \right],
\end{aligned}$$

whence

$$\mathbb{E}_{\tilde{Y}}[f_{S(\tilde{Y})|\tilde{Y}}(s)] = \sum_{k=0}^{\infty} (-s)^k \phi_{\tilde{B}}^{(k)} (1 - v_k) G_k(1|V). \tag{B.8}$$

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References

- [1] ANDERSSON, H. (1999), Epidemic models and social networks, *The Mathematical Scientist* **24** 128–147.
- [2] ANDERSSON, H. AND BRITTON, T. (2000), Stochastic epidemic models and their statistical analysis, *Springer Lecture Notes in Statistics* **151**, New York: Springer Verlag.
- [3] BALL, F.G. (2000), Susceptibility sets and the final outcome of stochastic SIR epidemic models, Research Report 00-09, Division of Statistics, School of Mathematical Sciences, University of Nottingham.
- [4] BALL, F.G.; MOLLISON, D. AND SCALIA-TOMBA, G. (1997), Epidemics with two levels of mixing, *Annals of Applied Probability* **7** 46–89.
- [5] BALL, F.G. AND NEAL, P.J. (2002), A general model for stochastic SIR epidemics with two levels of mixing, *Mathematical Biosciences* **180** 73–102.
- [6] BALL, F.G. AND O’NEILL, P.D. (1999), The distribution of general final state random variables for stochastic epidemic models, *Journal of Applied Probability* **36** 473–491.
- [7] BALL, F.G.; SIRL, D. AND TRAPMAN, P. (2009), Threshold behaviour and final outcome of an epidemic on a random network with household structure, *Advances in Applied Probability* **41** 765–796.
- [8] BALL, F.G.; SIRL, D. AND TRAPMAN, P. (2010), Analysis of a stochastic SIR epidemic on a random network incorporating household structure, *Mathematical Biosciences* **224** 53–73.
- [9] BOLLOBÁS, B.; JANSON, S. AND RIORDAN, O. (2007), The phase transition in inhomogeneous random graphs, *Random Structures and Algorithms* **31** 3–122.
- [10] BOLLOBÁS, B.; JANSON, S. AND RIORDAN, O. (2011), Sparse random graphs with clustering, *Random Structures and Algorithms* **38** 269–323.
- [11] BRITTON, T.; DEIJFEN, M.; LAGERÅS, A.N. AND LINDHOLM, M. (2008), Epidemics on random graphs with tunable clustering, *Journal of Applied Probability* **45** 743–756.
- [12] BRITTON, T.; JANSON, S. AND MARTIN-LÖF, A. (2007), Graphs with specified degree distributions, simple epidemics, and local vaccination strategies, *Advances in Applied Probability* **39** 922–948.
- [13] DALY, F. (1979) Collapsing supercritical branching processes, *Journal of Applied Probability* **16** 732–739.
- [14] DEIJFEN, M. AND KETS, W. (2009), Random intersection graphs with tunable degree distribution and clustering, *Probability in the Engineering and Informational Sciences* **23** 661–674.

- [15] DIEKMANN, O. AND HEESTERBEEK, J.A.P. (2000), *Mathematical Epidemiology of Infectious Diseases*, Chichester: John Wiley & Son.
- [16] DURRETT, R. (2006), *Random Graph Dynamics*, Cambridge University Press.
- [17] GLEESON, J.P. AND MELNIK, S. (2009), Analytical results for bond percolation and k-core sizes on clustered networks, *Physical Review E* **80** 046121.
- [18] GRIMMETT, G.R. AND STIRZAKER, D.R. (1992), *Probability and Random Processes (second edition)*, New York: Oxford University Press Inc.
- [19] GUPTA, B. (2008) Number of edges in random intersection graph on surface of a sphere, preprint: arXiv:0809.1143v1.
- [20] JAGERS, P. (1975), *Branching Processes with Biological Applications*, London: John Wiley & Sons.
- [21] JAWORSKI, J.; REN, M. AND RYBARCZYK, K. (2009), Random key predistribution for wireless sensor networks using deployment knowledge, *Computing* **85** 57–76.
- [22] KARONSKI, M. SCHEINERMAN, E.R. AND SINGER-COHEN, K.B. (1999), On Random Intersection Graphs: The Subgraph Problem, *Combinatorics, Probability and Computing* **8** 131–159.
- [23] MOLLOY, M. AND REED, B. (1995), A critical point for random graphs with a given degree sequence, *Random Structures and Algorithms* **6** 161–180.
- [24] NERMAN, O. (1981), On the convergence of supercritical general (C-M-J) branching processes, *Zeitschrift für Wahrscheinlichkeitstheorie und verwandte Gebiete* **57** 365–395.
- [25] NEWMAN, M.E.J. (2002), Spread of epidemic disease on networks, *Physical Review E* **66** 016128.
- [26] NEWMAN, M.E.J. (2003), Properties of highly clustered networks, *Physical Review E* **68** 026121.
- [27] NEWMAN, M.E.J. (2009), Random graphs with clustering, *Physical Review Letters*, **103** 058701.
- [28] NORROS, I. AND REITTU, H. (2006), On a conditionally Poissonian graph process, *Advances in Applied Probability* **38** 59–75.
- [29] PELLIS, L.; BALL, F.G. AND TRAPMAN, P. (2012), Reproduction numbers for epidemic models with households and other social structures. I. Definition and calculation of R_0 , *Mathematical Biosciences* **235** 85–97.
- [30] PENROSE, M. (2003), *Random geometric graphs*, Oxford University Press, Oxford.
- [31] PICARD, P. AND LEFÈVRE, C. (1990), A unified analysis of the final size and severity distribution in collective Reed-Frost epidemic processes, *Advances in Applied Probability* **22** 269–294.

- [32] RASCH, G. (1961), On general laws and the meaning of measurement in psychology, in *Proceedings of the Fourth Berkeley Symposium on Mathematical Statistics and Probability, IV* 321?–334
- [33] RIORDAN, O. (2005), The small giant component in scale-free random graphs, *Combinatorics, Probability and Computing* **14** 897–938.
- [34] SHANG, Y. (2010), Degree distributions in general random intersection graphs, *Electronic Journal of Combinatorics* R23.